

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 11, 2004, 13:53:18 ; Search time 2407.08 Seconds
(without alignment)
234.084 Million cell updates/sec

Title: US-09-444-281-35
Perfect score: 91
Sequence: 1 ILKCKWPWPNRK 13

Scoring table: BL05UM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=0/2.1/USPTO_spool/US944221/runat_07052004_171138_2568/app_query.fasta_1..398
-DB=GenEnt1 -QENT=fastap -SUFIXX=rge -MINMATCH=0..1 -LOOPFCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bioum62 -TRANS=human40_cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pcT IFR MAX=100 -THR MIN=0 -ALIGN=100 -NODE=LOCAL
-OUTPNT=pcO -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09442281 @CGN 1..3608 @runat 07052004_171138_2568 -ICPU=6 -ICPU=3
-NO_NMA -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPEXT=0.5 -FGAPEXT=7
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELET=7

Database :

GenEnt1 :
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2: gb_ntg:
3: gb_in:
4: gb_cm:
5: gb_ov:
6: gb_sts:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_dat:
12: gb_sy:
13: gb_un:
14: gb_vn:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_om:
21: em_or:
22: em_ov:
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24: em_bh:
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26: em_ro:
27: em_sts:
28: em_un:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	91	100.0	114	6	BD247517	BD247517 Method fo
2	76	83.5	108	6	BD247523	BD247523 Method fo
3	76	83.5	114	6	BD247529	BD247529 Method fo
4	76	83.5	151	6	BD247520	BD247520 Method fo
5	73	80.2	39	6	BD128612	BD128612 Method fo
6	73	80.2	68	6	AX357080	Sequence AX357080
7	73	80.2	69	6	AR404925	Sequence AR404925
8	73	80.2	211	6	AR222388	Sequence AR222388
9	73	80.2	211	6	AR282754	Sequence X67310 Bos taurus
10	73	80.2	550	4	BTINDLCD	BTINDLCD
11	73	80.2	6446	6	BR173324	BR173324 Sequence AR173324
12	73	80.2	6446	6	AX098418	AX098418 Sequence AX098418
13	69	75.8	156785	2	AC146517	AC146517 Homo sapi
14	69	75.8	157518	9	AC093525	AC093525 Homo sapi
15	69	75.8	176552	9	AC106820	AC106820 Homo sapi
16	69	75.8	205268	2	AC146518	AC146518 Homo sapi
17	68	74.7	141040	8	AP004382	AP004382 Oryza sat
18	67	73.6	195764	2	AC113900	AC113900 Rattus no
19	67	73.6	228163	2	AC120671	AC120671 Rattus no
20	67	73.6	241568	2	AC129646	AC129646 Rattus no
21	67	73.6	255121	2	AC095460	AC095460 Rattus no
22	66	72.5	207	6	BD273664	BD273664 Peptides
23	66	72.5	2651	10	MM0108210	MM0108210
24	66	72.5	3643	10	BC051649	BC051649 Mus muscu
25	66	72.5	65209	2	AC101355	AC101355 Mus muscu
26	66	72.5	107257	10	AF289665	AF289665 Mus muscu
27	66	72.5	146408	8	AC130610	AC130610 Oryza sat
28	66	72.5	175454	2	AC127242	AC127242 Mus muscu
29	66	72.5	179914	10	AC124511	AC124511 Mus muscu
30	66	72.5	201395	10	AC091250	AC091250 Mus muscu
31	65	71.4	233522	2	AC101355	AC101355 Mus muscu
32	65	71.4	27780	2	AC020365	AC020365 Drosophil
33	65	71.4	110000	2	BX255276_07	Continuation (8 f
34	65	71.4	149951	10	AL672300	AL672300 Mouse DNA
35	65	71.4	160817	3	AC008316	AC008316 Drosophil
36	65	71.4	177028	3	AC008315	AC008315 Drosophil
37	65	71.4	23823	3	AC11774	AC11774 Mus muscu
38	65	71.4	23823	3	CAC300832	CAC300832
39	65	71.4	269559	2	AE003684	AE003684 Drosophil
40	65	71.4	30132	1	AC093467	AC093467 Mus muscu
41	64	70.3	39	6	BD273655	BD273655 Peptides
42	64	70.3	53	6	BD273657	BD273657 Peptides
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44	64	70.3	2718	10	BC029697	BC029697 Mus muscu
45	64	70.3	19479	10	Z22923	Z22923 M. musculus

ALIGNMENTS

RESULT 1

BD247517 LOCUS BD247517 114 bp linear PAT 17-JUL-2003 DEFINITION Method for effectively producing antibacterial cationic peptides in host cells.

ACCESSION BD247517 VERSION BD247517.1 (GL:33057287 KEYWORDS JP 2002530114-A/11. synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 114) Burian,J. and Bartfeld,D.

AUTHORS Method for effectively producing antibacterial cationic peptides in host cells

JOURNAL PATENT: JP 2002530114-A 11 17-SEP-2002;

COMMENT OS Artificial Sequence

PN JP 2002530114-A/11

PD 17-SEP-2002

PF 19-NOV-1999 JP 2000584088

PR 20-NOV-1998 US 60/109218

PI JAN BURIAN, DANIEL BARTFIELD

PC C12N15/09, C07K1/12, C07K1/18, C12N1/19, C12N1/21, C12P21/02//

PC (C12P21/02, C12R1:19) C12N15/00

CC Synthesized oligonucleotide used as a template for PCR

Key FT source 1..114 /organism='Artificial Sequence'

FT Location/Qualifiers 1..114 /organism='Artificial Sequence'

FEATURES Source 1..114 /organism='Artificial Sequence'

1..114 /organism='Synthetic construct'

/mol type="genomic DNA"

/db_xref="taxon:32630"

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Pred. No.: 0.047 Length: 114

Score: 91.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-444-281-35 (1-13) x BD247517 (1-108)

QY 1 IleLeuLysTyrProTyrProTyrArgArgLys 13

Db 38 ATGATTCCTGCCTTGCCTGCCCTGCTGGCGCTGCGTCGAAA 76

RESULT 3 BD247529 LOCUS BD247529 114 bp DNA linear PAT 17-JUL-2003 DEFINITION Method for effectively producing antibacterial cationic peptides in host cells.

ACCESSION BD247529 VERSION BD247529.1 GI:33057299

KEYWORDS JP 2002530114-A/23.

SOURCE OS Artificial Sequence

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 114)

AUTHORS Burian,J. and Bartfeld,D.

TITLE Method for effectively producing antibacterial cationic peptides in host cells

JOURNAL PATENT: JP 2002530114-A 23 17-SEP-2002;

COMMENT OS Artificial Sequence

PN JP 2002530114-A/23

PD 17-SEP-002

PF 19-NOV-1999 JP 2000584088

PR 20-NOV-1998 US 60/109218

PI JAN BURIAN, DANIEL BARTFIELD

PC C12N15/09, C07K1/12, C07K1/18, C12N1/15, C12N1/19, C12N1/21, C12P21/02//

PC (C12P21/02, C12R1:19) C12N15/00

CC Synthesized oligonucleotide used as a template for PCR

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1..114 /organism='Synthetic construct'

/mol type="genomic DNA"

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Pred. No.: 0.262 Length: 114

Score: 76.00 Matches: 9

Percent Similarity: 92.31%

Best Local Similarity: 69.23%

Query Match: 83.52%

DB: 6 Gaps: 0

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QY 1 IleleuIysLysTPrOrnTPrOrnTPrOrnTPrOrnTPrArgLys 13	PN	JP 200502246-A/15	
Db 44 ATGATTCCTCGCTGGCGTGGCTGCGCTGGGTGCGCAA 82	PD	22-JAN-2002	
RESULT 4	PF	28-MAY-1998 JP 199500514	
LOCUS BD247520	PR	28-MAY-1997 KR 199721312,09-APR-1998 KR 199813372 PI	
DEFINITION Method for effectively producing antibacterial cationic peptides in host cells.	PI	SUN CHANG KIM, JAE HYUN LEE, MIN HYUNG KANG, JEONG HYUN KIM, SEUNG PI SUH HONG,	
ACCESSION BP247520	PC	HYUN SOO LEE	
VERSION JP 2005030114-A/14	CC	C12N15/62	
KEYWORDS synthetic construct	Method for mass production of antimicrobial peptide		
ORGANISM synthetic construct	Key		
REFERENCE 1 (bases 1 to 151)	FT	Location/Qualifiers	
AUTHORS Burian,J. and Bartfeld,D.	FT	1. .39	
TITLE Method for effectively producing antibacterial cationic peptides in host cells	FEATURES	Location/Qualifiers	
JOURNAL Patent:JP 2005030114 A 14 17-SEP-2002;	source	1. .39	
COMMENT MICROGIX BIOTECH INC	source		
OS Artificial Sequence	source		
PN GP 2005030114-A/14	source		
PD 17-SEP-2002	source		
PF 19-NOV-1999 JP 20000584088	source		
PR 20-NOV-1998 US 60/102318	source		
PI JAN BURIAN, DANIEL BARTFELD	source		
PC C12N15/09, C07K1/12, C07K1/18, C12N1/19, C12N1/21, C12P21/02 //	source		
PC (C12P21/02, C12R1/19), C12N15/00	source		
CC synthesized oligonucleotide used as a template for PCR	source		
Key	FT	Location/Qualifiers	
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Percent Similarity: 92.31%	source		
Best Local Similarity: 63.23%	source		
Query Match: 83.52%	source		
DB: 6	source		
US-09-444-281-35 (1-13) x BD247520 (1-151)	source		
QY 1 IleleuIysLysTPrOrnTPrOrnTPrOrnTPrOrnTPrArgLys 13	QY	4 LysTPrOrnTPrOrnTPrOrnTPrArgLys 13	
Db 38 ATGATTCCTCGCTGGCGTGGCTGCGCTGGGTGCGCAA 76	Db	31 AAATGGCTTGGCTGCGCTGGGTGCGCAA 76	
RESULT 5	FEATURES	Location/Qualifiers	
LOCUS BD128612	source	1. .68	
DEFINITION Method for mass production of antimicrobial peptide.	source		
ACCESSION BD128612	source		
VERSION BD128612.1	source		
KEYWORDS JP 200503246-A/15.	source		
SOURCE unidentified	source		
ORGANISM unidentified	source		
REFERENCE 1 (bases 1 to 39)	source		
AUTHORS Kim,S.-C., Lee,J.-H., Kang,M.-H., Kim,J.-H., Hong,S.-S. and Lee,H.-S.	source		
TITLE Method for mass production of antimicrobial Peptide	source		
JOURNAL Patent: JP 200503246 A 15 22-JAN-2002;	source		
SAMYANG GENEX CORP., KOREA ADVANCED INSTITUTE OF SCIENCE AND TECHNOLOGY	source		
COMMENT OS	Alignment Scores:		
PN JP 200502246-A/15	Pred. No. :	0.347	
PD 22-JAN-2002	Score:	73.00	
PF 28-MAY-1998 JP 199500514	Percent Similarity:	100.00%	
PR 28-MAY-1997 KR 199721312,09-APR-1998 KR 199813372 PI	Best Local Similarity:	100.00%	
PI SUN CHANG KIM, JAE HYUN LEE, MIN HYUNG KANG, JEONG HYUN KIM, SEUNG PI SUH HONG,	Query Match:	80.22%	
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PI HYUN SOO LEE	Conservative:	0	
PC C12N15/62	Mismatches:	0	
CC Method for mass production of antimicrobial peptide	Indels:	0	
PI HYUN SOO LEE	Gaps:	0	
PC C12N15/62	Comments:	0	
CC Method for mass production of antimicrobial peptide	Mismatches:	0	
PI HYUN SOO LEE	Indels:	0	
PC C12N15/62	Length:	68	
CC Method for mass production of antimicrobial peptide	Matches:	9	
PI HYUN SOO LEE	Conservative:	0	
PC C12N15/62	Mismatches:	0	
CC Method for mass production of antimicrobial peptide	Indels:	0	
PI HYUN SOO LEE	Gaps:	0	
PC C12N15/62	Comments:	0	
CC Method for mass production of antimicrobial peptide	Mismatches:	0	
PI HYUN SOO LEE	Indels:	0	
PC C12N15/62			

RESULT 7
AR40425 AR40425 69 bp DNA linear PAT 18-DEC-2003
LOCUS Sequence 1 from patent US 6630197.
DEFINITION
ACCESSION AR40425
VERSION GI:40153719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 69)
AUTHORS Wood,T.K., Jayaram,A. and Barthman,J.C.
TITLE Inhibition of sulfate-reducing-bacteria-mediated degradation using
bacteria which secrete antimicrobials
PATENT US 6630197-A 07-OCT-2003;
JOURNAL
FEATURES Location/Qualifiers
1. .69
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.352 Length: 69
Score: 73.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00%
Query Match: 80.22% Indels: 0
DB: 6 Gaps: 0
US-09-444-281-35 (1-13) x AR404925 (1-69)
QY 4 LysTrpProTrpTrpProTrpArgArg 12
Db 28 AAATGGCTTGTGGCCCTTGGGGCCGC 54
RESULT 8
AR226388 AR226388 211 bp DNA linear PAT 20-DEC-2002
LOCUS Sequence 11 from patent US 6444645.
DEFINITION
ACCESSION AR226388
VERSION GI:27264888
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 211)
AUTHORS Selsted,M.E. and Osapay,K.
TITLE Crosslink-stabilized indolicidin analogs
PATENT US 6444645-A 11 03-SEP-2002;
JOURNAL
FEATURES Location/Qualifiers
1. .211
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.13 Length: 211
Score: 73.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00%
Query Match: 80.22% Indels: 0
DB: 6 Gaps: 0
US-09-444-281-35 (1-13) x AR226388 (1-211)
QY 4 LysTrpProTrpTrpProTrpArgArg 12
Db 38 AAATGGCTTGTGGCCCTTGGGGCCGC 64
RESULT 9
AR282754 AR282754 211 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 38 from patent US 6524585.
DEFINITION

ACCESSION AR282754
VERSION AR282754-1
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 211)
AUTHORS Selsted,M.E.
TITLE Indolicidin analogs and methods of using same
JOURNAL Patent: US 6524585-A 28-FEB-2003;
FEATURES Location/Qualifiers
source 1. .211
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.13 Length: 211
Score: 73.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00%
Query Match: 80.22% Indels: 0
DB: 6 Gaps: 0
US-09-444-281-35 (1-13) x AR282754 (1-211)
QY 4 LysTrpProTrpTrpProTrpArgArg 12
Db 38 AAATGGCTTGTGGCCCTTGGGGCCGC 64
RESULT 10
BTINDLCD BTINDLCD 550 bp mRNA linear MAM 15-NOV-2001
LOCUS BTINDLCD mRNA for cathelicidin (CATHL4 gene).
DEFINITION Bos taurus mRNA for cathelicidin (CATHL4 gene).
ACCESSION X67340
VERSION X67340-1
KEYWORDS cathelicidin; CATHL4 gene; indolicidin antimicrobial peptide.
ORGANISM Bos taurus (cow)
Bovidae; Bovinae; Bos
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buteraria; Catariodiocyla; Ruminantia; Pecora; Bovoidea;
Valerio, 38, 34127 Trieste, ITALY
REFERENCE 1
AUTHORS Del Sal,G., Storici,P., Schneider,C., Romeo,D. and Zanetti,M.
TITLE cDNA cloning of the neutrophil bactericidal peptide indolicidin
JOURNAL Biochem. Biophys. Res. Commun. 187 (1), 467-472 (1992)
MEDLINE 15203368
PUBMED 15203368
REFERENCE 2 (bases 1 to 550)
AUTHORS Del Sal,G.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-1992) G. Del Sal, Univ. of Trieste, Dip. di
Biochimica, Biofisica e Chimica delle Macromolecole, Via A.
Valerio, 38, 34127 Trieste, ITALY
FEATURES Location/Qualifiers
source 1. .550
/organism="Bos taurus"
/function="indolicidin antimicrobial peptide"
/mol_type="mRNA"
/codon_start-1
/product="cathelicidin"
/protein_id="CA44775-1"
/db_xref="GI:463"
/db_xref="Gor:P33046"
/db_xref="SWISS-PROT:P33046"
/translation "MOTORSLISGRISIWLILGLVYPSASAQLSYRAVLRAVDQ
LINEUSSEANLYRILEDPPFKDNEDLGRDKVPSFTVKRTICQAEQCDKEKG

*	2430	3567: contig of 1138 bp in length	Direct Submission	TITLE
*	3568	3667: gap of unknown length	Submitted (04-DEC-2002)	JOURNAL
*	3668	4716: contig of 1049 bp in length	Drive, Walnut Creek, CA 94598, USA	
*	4816	4817: gap of unknown length	On Dec 4, 2002 this sequence version replaced gi:1601346.	COMMENT
*	7813	7812: contig of 2996 bp in length	Draft Sequence Produced by DOE Joint Genome Institute	
*	7912	7912: gap of unknown length	www.jgi.doe.gov	
*	14712	14712: contig of 6800 bp in length	Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory	
*	14813	14813: contig of 4849 bp in length	www.shgc.stanford.edu	
*	19662	19662: gap of unknown length	Quality: Phrap Quality >=0 99.9% of Sequence;	
*	24662	24662: contig of 4901 bp in length	Estimated Total Number of Errors is 0.2.	
*	24663	24663: gap of unknown length	Location/Qualifiers	
*	24763	24763: contig of 9378 bp in length	1. 1.157518	
*	34140	34140: gap of unknown length	/organism="Homo sapiens"	
*	34141	34141: contig of 9113 bp in length	/mol_type="genomic DNA"	
*	43241	43241: gap of unknown length	/db_xref="taxon:1606"	
*	43253	43253: contig of 15825 bp in length	/chromosome="16"	
*	43454	43454: gap of unknown length	/clone="RP11-20123"	
*	56333	56333: gap of unknown length		
*	56434	56434: contig of 17790 bp in length		
*	74223	74223: gap of unknown length		
*	74224	74224: contig of 15825 bp in length		
*	90148	90148: gap of unknown length		
*	90249	90249: contig of 23908 bp in length		
*	91456	91456: gap of unknown length		
*	114257	114257: gap of unknown length		
*	114257	114257: contig of 42529 bp in length.		
FEATURES		Location/Qualifiers		
Source	1..156785			
ORIGIN				
Alignment Scores:				
Pred. No.:	3.38e+03	Length:	3.4e+03	
Score:	69.00	Matches:	69..00	
Percent Similarity:	91.67%	Percent Similarity:	91.67%	
Best Local Similarity:	83.33%	Best Local Similarity:	83.33%	
Query Match:	75.82%	Query Match:	75.82%	
DB:	2	DB:	9	
US-09-444-281-35 (1-13) x AC093525 (1-157518)				
Qy	2 LeuLysLysTrpProTrpProTrpArgArgLys 13			
Db	106227 TTACAAAAATCCCTGGGCCCTGGAGGAAG 106262			
RESULT 15				
AC106820				
LOCUS	AC106820	176552 bp	DNA	linear
DEFINITION	Homo sapiens chromosome 16 c1one	RP11-715J22	complete sequence.	
ACCESSION	AC106820			
VERSION	AC106820.4			
KEYWORDS	HTG..			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Butheria; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 17652)			
AUTHORS	DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.			
TITLE	Direct Submission			
REFERENCE	2 (bases 1 to 176552)			
AUTHORS	DOE Joint Genome Institute.			
TITLE	Direct Submission			
JOURNAL	Submitted (12-JAN-2002)			
GENOME INSTITUTE	Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
REFERENCE	3 (bases 1 to 176552)			
AUTHORS	DOE Joint Genome Institute.			
TITLE	Direct Submission			
JOURNAL	Submitted (27-MAR-2002)			
GENOME INSTITUTE	Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
REFERENCE	4 (bases 1 to 176552)			
AUTHORS	DOE Joint Genome Institute.			
TITLE	Direct Submission			
JOURNAL	Submitted (02-JUL-2002)			
GENOME INSTITUTE	Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
REFERENCE	5 (bases 1 to 176552)			
AUTHORS	DOE Joint Genome Institute and Los Alamos National Laboratory.			
TITLE	Direct Submission			
JOURNAL	Submitted (26-NOV-2003)			
GENOME INSTITUTE	Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
REFERENCE	On Nov 26, 2003 this sequence version replaced gi:21672112.			
AUTHORS	Draft Sequence Produced by DOE Joint Genome Institute			
COMMENT				

www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www.shgc.stanford.edu
Quality: Phrap Quality ≥ 40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
FEATURES
Source
1. 176552
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
/clone="RP11-715J22"
ORIGIN

Alignment Scores:
Pred. No.: 3.83e+03 Length: 176552
Score: 69.00 Matches: 10
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 1
Query Match: 75.82% Indels: 0
DB: 9 Gaps: 0

US-09-444-281-35 (1-13) \times AC106820 (1-176552)
Qy 2 LeuLysTrpProTrpTrpProTrpArgArgLys 13
Db 16954 TRACAAAATCCCCCTGGTGGCCCTGGAGGAG 16989

Search completed: May 11, 2004, 16:01:29
Job time : 2429.08 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 11, 2004, 12:39:07 ; Search time 256.88 Seconds
(without alignments)
214.990 Million cell updates/sec

Title: US-09-444-281-35
Perfect score: 91
Sequence: 1 TLKXPPWWFWRK 13

Scoring table: BLOSUM62
Xgapext 0.0 , Xgapext 0.5
Ygapext 10.0 , Ygapext 0.5
Fgap 6.0 , Fgapext 7.0
DelOp 6.0 , Delext 7.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+P2N.n.model -DEV=>xh
-Q=cgn_1/USP10_sp01/runat 070502004_171138_2561/app_query.fasta_1.398
-DB=N Geneseq_29Jan04 -QFMT=fastap -SUFFIX=x-rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=8-bits -START=-1 -END=-1 -MATPIK=0globum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=PCP -THR MAX=100 -THR MIN=0 -ALIGN=15
-USER=US09444281 @cgn_1.586 @runat 070502004_171138_2561_NCP0-6 -ICPU=3
-NO_MMW -LARGEQUERY -NEG SCORE=1 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -TREAINS=1 -XGAPOP=0 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=0 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_29Jan04 :*

1: geneseqn1980b :*
2: geneseqn1990b :*
3: geneseqn2000b :*
4: geneseqn2001ab :*
5: geneseqn2001bs :*
6: geneseqn2002b :*
7: geneseqn2003ab :*
8: geneseqn2003bs :*
9: geneseqn2003cs :*
10: geneseqn2004s :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	91	100.0	88	2	AAV60908	Aav60908 DNA fragm
2	91	100.0	114	3	AAA27291	Aaa27291 Oligonucle
3	76	83.5	108	3	AAA27296	Aaa27296 Oligonucle
4	76	83.5	114	3	AAA27298	Aaa27298 Oligonucle
5	76	83.5	151	3	AAA27294	Aaa27294 Oligonucle
6	73	80.2	39	2	AAV83788	Aav83788 Antimicro
7	73	80.2	47	3	AAZ23389	Aaz23389 PCR prime
C	73	80.2	47	3	AAZ23390	Aaz23390 PCR prime

Abi60414 DNA fragm
Abi60415 DNA fragm
Abi60416 Antimicro
Abi60441 DNA fragm
Abi60445 DNA fragm
Aai172481 cDNA deri
Aai772481 Oligonucle
Aaz19764 Oligonucle
Aaz45123 Indolicid
Aad15350 Cow artici
Aaz23347 TNV-based
Aaa28519 PCR1 DNA
Abi121539 Drosophili
Abi121536 Drosophili
Aaa28510 Rev4 codi
Adc73315 Antibacte
Adc73331 Tobacco P
Adc73339 Magainin
Abi158680 Mouse X-t
Abi96610 Mouse X-t
Aba96610 Pseudomon
Aaa4129 Pseudomon
Aab6109 Salmonall
Aaa28514 Pro-nagai
Aaa28512 Primer RI
Aca51647 Prokaryot
Abc52723 Primary r
Aaa27290 Antisense
Aaa27287 Oligonucle
Aaa28514 Pro-nagai
Aaa28512 Primer RI
Abc94411 Rice endo
Aat60750 Pseudomona
Ada70241 Rice Gene
Abi122542 Drosophili
Abc8177 Human ost
Aab84495 Mouse alp
Aab84495 Mouse alp
Aab61792 Human GPC
Aab61792 Human GPC
Adb02891 Mouse Blr
Adb72629 Mouse Blr

ALIGNMENTS

RESULT 1

XX	AAV60908	standard; DNA; 88 BP.
ID	AAV60908	
XX	AAV60908;	
AC		
XX		
DT	11-JAN-1999	(first entry)
XX		
DE		DNA fragment encoding MB11.
XX		
DE		
XX		
DE		
XX		
DE		
XX		
DE		
XX		
OS		Synthetic.
OS		Homo sapiens.
XX		
PN	W0841636-A2.	
XX		
PA	(BUR1/)	BURIAN J.
XX		(KAYW/)
PA		KAY W W.
XX		
PT		Burian J, Kay WW;
XX		
DR	WPI; 1998-531571/45.	
XX		

Increasing plasmid copy number in a cell with the repa gene product - and

PT an small cryptic plasmid ori sequence, useful for high level expression
 PT of e.g. cytokines, antigens or therapeutic proteins.
 XX

Example 16; Page 57; 82pp; English.

XX This oligonucleotide was used as a template in a PCR reaction (see also AAV60309-1C) to generate a DNA fragment encoding the cationic peptide MBI-11 (see AAV71690). The PCR product was cloned into the universal vector pRCh-B1, which contains the R21 replication leader of RepA (see AAV71696) and 2 tandem copies of the prepro region (Aprl) of human defensins. The vector provides expression of R21-hpro-MBI-11 fusion in host cells. The invention provides controlled replication plasmid vectors (FAMP vectors), comprising a replication origin of a small cryptic plasmid such as pKL1 (see AAV71696) and a gene encoding RepA (see AAV71696). The vectors can reach very high levels of plasmid replication, but are not lethal to the host cell, and can be used to direct the high level expression of e.g. cytokines, antigens and therapeutic proteins

SQ Sequence 88 BP; 20 A; 18 C; 25 G; 25 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.00318 Length: 88
 Score: 91.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-444-281-35 (1-13) x AAV60908 (1-8)

QY 1 IleLeuLysLysTrpProTrpProTrpProTrpProTrpArgArgLys 13
 Db 25 ATCCGAAAAATGGCTGTTGCGCNGGGCTGATAA 63

RESULT 2

AA27291 ID AAV60908 standard; DNA; 114 BP.
 XX AC AA27291;

XX DT 20-SEP-2000 (first entry)

XX Oligonucleotide used for synthesis of MBI-11 fragment.

XX DE 20-NOV-1998; 99WO-CA001107.
 XX KW Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11;
 XX KW indolicidin; bovine; ss.
 XX OS Synthetic.
 XX PN WO20031279-A2.
 XX DR 2000-400086/34.

XX PT Multi-domain fusion protein expression cassette used for high yield
 XX PT stable production of foreign peptide gene products.
 XX PS Example 5; Page 39; 73pp; English.

XX XX A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic Peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin

XX PA (MICR-) MICROLOGIX BIOTECH INC.
 XX PI Burian, J., Bartfeld, D;
 XX DR 2000-400086/34.
 XX PT Multi-domain fusion protein expression cassette used for high yield
 XX PT stable production of foreign peptide gene products.
 XX PS Example 4; Page 37; 73pp; English.

XX XX A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the

CC positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11 fragment. MBI-11 is a cationic peptide derived from modifications of indolicidin

XX Sequence 114 BP; 25 A; 26 C; 30 G; 33 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 0.00421 Length: 114
 Score: 91.00 Matches: 13
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-444-281-35 (1-13) x AAA27291 (1-114)

QY 1 IleLeuLysLysTrpProTrpProTrpProTrpProTrpProTrpArgArgLys 13

Db 41 ATCCGAAAAATGGCTGTTGCGCNGGGCTGCTGCTGAA 79

RESULT 3

AA27296

ID AAA27296 standard; DNA; 108 BP.

XX XX

AC AAA27296;

XX DT 20-SEP-2000 (first entry)

XX DE Oligonucleotide used for synthesis of MBI 2X11B7 poly cassette.

XX XX

KW Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11;

XX KW indolicidin; bovine; ss.

XX OS Synthetic.

XX PN WO20031279-A2.

XX DR 2000-400086/34.

XX PT Multi-domain fusion protein expression cassette used for high yield

XX PT stable production of foreign peptide gene products.

XX PS Example 5; Page 39; 73pp; English.

XX XX A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic Peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin

XX SQ Sequence 108 BP; 18 A; 33 C; 31 G; 26 T; 0 U; 0 Other;

XX Alignment Scores:

XX XX A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic Peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11 fragment. MBI-11 is a cationic peptide derived from modifications of indolicidin

XX SQ Sequence 108 BP; 18 A; 33 C; 31 G; 26 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No. :	0-251	Length:	108 .
Score:	76.00	Matches:	9
Percent Similarity:	92.31%	Conservative:	3
Best Local Similarity:	69.23%	Mismatches:	1
Query Match:	83.52%	Indels:	0
DB:	3	Gaps:	0
US-09-444-281-35 (1-13) x AAA27296 (1-108)			
QY	1 IleLeuLysTrpProTrpProTrpArgArgLys 13		
DB	38 ATGATTCGCGTGGCGTGGCGCTGCGCTGGCAA 76		
RESULT 4			
ID	AAA27298 standard; DNA; 114 BP.		
XX			
AC	AAA27298;		
XX			
DT	20-SEP-2000 (first entry)		
DB	Oligonucleotide used for synthesis of MBI 11B7 first cassette.		
XX			
DB	Oligonucleotide used for synthesis of MBI 2X11B7 last cassette.		
XX			
DB	Oligonucleotide used for synthesis of MBI 2X11B7 last cassette.		
XX			
DB	Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11;		
XX			
DB	KW indolicidin; bovine; ss.		
XX			
OS	Synthetic.		
XX			
PA	(MICR-) MICROLOGIX BIOTECH INC.		
XX			
PA	Burian J, Bartfeld D;		
XX			
PN	WO20031279-A2.		
XX			
PD	WPI; 2000-400086/34.		
XX			
DT	02-JUN-2000.		
XX			
PP	99WO-CA001107.		
XX			
PR	19-NOV-1999;		
XX			
PR	99US-0109218P.		
XX			
PR	20-NOV-1998;		
XX			
PS	98US-0109218P.		
XX			
PA	(MICR-) MICROLOGIX BIOTECH INC.		
XX			
PA	Burian J, Bartfeld D;		
XX			
PI	WPI; 2000-400086/34.		
XX			
DR	Multi-domain fusion protein expression cassette used for high yield		
XX			
PT	stable production of foreign peptide gene products.		
XX			
PT	Example 5; Page 40; 73pp; English.		
XX			
PT	A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin		
XX			
SQ	Sequence 151 BP; 22 A; 44 C; 49 G; 36 T; 0 U; 0 Other;		
XX			
PS	Sequence 114 BP; 20 A; 34 C; 32 G; 28 T; 0 U; 0 Other;		
XX			
PS	Alignment Scores:		
Pred. No. :	0-266	Length:	114
Score:	76.00	Matches:	9
Percent Similarity:	92.31%	Conservative:	3
Best Local Similarity:	69.23%	Mismatches:	1
Query Match:	83.52%	Indels:	0
DB:	3	Gaps:	0
US-09-444-281-35 (1-13) x AAA27298 (1-114)			
QY	1 IleLeuLysTrpProTrpProTrpArgArgLys 13		
DB	38 ATGATTCGCGTGGCGCTGGCGTGGCGTGGCAA 76		
RESULT 6			
ID	AAV83788		
XX	AAV83788 standard; DNA; 39 BP.		
AC	AAV83788;		
XX			
DT	19-MAR-1999 (first entry)		

purF gene; fusion peptide; mass production; pharmaceutical industry;
food industry; ss.

Synthetic.
OS

XX

W09864611-A1.

XX

16-DEC-1999.

XX

PF 08-JUN-1999;

99W0-KR002822.

XX

PR 09-JUN-1998;

98KR-00022117.

XX

PR 14-MAY-1999;

99KR-00017920.

XX

(SAMY-) SAMYANG GENEX CORP.

XX

Kim JH, Kang MH, Lee JW, Hong SS, Lee H;

PS Example 1; Page 13; 67pp; English.

XX

WPI; 2000-097542/08.

XX

XX The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purF gene or its derivative, and a second gene sequence which codes peptide antibiotics. The mass-production method of peptide antibiotics comprises the steps of; constructing an expression vector including the genetic component, transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of pEX2, pGEX2, pGEX4 and pGEX5, and it has a high copy number of origin, strong transcription promoter and structural gene. The sequences given in records ABL60400-ABL60464 represent DNA sequences of the invention

XX Sequence 47 EP; 12 A; 18 C; 10 G; 7 T; 0 U; 0 Other;

SQ Alignment Scores:
Pred. No.: 0.2355 Length: 47
Score: 73.00 Matches: 9
Percent. Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 60.00% Indels: 0
DB: 6 Gaps: 0

US-09-444-281-35 (1-13) x ABL60415 (1-47)

QY 4 LysTrpProTrpProTrpProTrpArg 12
DB 35 AAATGGCGGTGGCGCTGGCTGT 9

RESULT 11
AAZ29364

ID AAZ29364 standard; DNA; 53 BP.

XX AC AAZ29364;

XX DT 29-FEB-2000 (first entry)

XX DE Antimicrobial peptide, Indolicidin encoding DNA.

XX KW purF gene; glutamine pyrophosphoryl pyrophosphate amidotransferase;
XX KW purF derivative; fusion partner; antimicrobial peptide; Indolicidin;
XX KW mass production; cleavage site; hydroxylamine; CNBr; DNA construct; cow;
XX KW neutralise; toxicity; pharmaceutical industry; food industry; ds.
XX OS Bos taurus.

XX FH Key Location/Qualifiers
CBS 5 .46 /*tag= a
FT /product= "Indolicidin peptide" used in DNA construct"
FT /note= "Antimicrobial peptide used in DNA construct"
XX PN WO9964611-A1.

XX PD 16-DEC-1999.

XX PF 08-JUN-1999; 99WO-KR000282.

XX PR 09-JUN-1998; 98KR-00021117.

XX PR 14-MAY-1999; 99KR-00017920.

XX PA (SAMY-) SANYANG GENEX CORP.

XX PI Kim JH, Kang MH, Lee J, Park SH, Lee JW, Hong SS, Lee H;

XX DR WPI; 2000-097542/08.

XX DR P-PSDB, AAY44424.

XX PT New DNA constructs useful for mass production of antimicrobial peptides in microorganism hosts.
PT PT PT
XX

ES Claim 1; Fig 1; 67pp; English.

XX The present DNA sequence encodes an antimicrobial peptide, Indolicidin derived from cow, Bos taurus. It is used along with a derivative of purF gene sequence that functions as a fusion partner. A DNA construct that comprises, this antimicrobial peptide encoding sequence and the entire, partial or derivative of purF gene, is used for mass production of the antimicrobial peptide in microorganisms without killing the host cells. Use of the purF gene derivative sequence, neutralises the toxicity of the antimicrobial peptides against the host microorganisms. The antimicrobial peptides are useful commercially in the pharmaceutical and food industries

XX Sequence 53 BP; 8 A; 12 C; 20 G; 13 T; 0 U; 0 Other;

SQ Alignment Scores:
Pred. No.: 0.267 Length: 53
Score: 73.00 Matches: 9
Percent. Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 80.22% Indels: 0
DB: 3 Gaps: 0

US-09-444-281-35 (1-13) x AAZ29364 (1-53)

QY 4 LysTrpProTrpProTrpProTrpArg 12
DB 17 AAATGGCGGTGGCGTGGCGTGGCGTGT 43

RESULT 12
ID ABL60445 standard; DNA; 53 BP.

XX AC ABL60445;

XX DT 28-MAR-2003 (first entry)

XX DE DNA fragment of the invention #44.

XX Gene expression; peptide antibiotic; purF gene; ds.
XX OS Unidentified.
XX FH Key Location/Qualifiers
CDS 5 .60 /*tag= a
FT ET /partial
FT ET /note= "no start codon present"
XX AX PN KR2001098973-A.
XX PD 08-NOV-2001.
XX PP 08-JUN-2001; 2001KRR-00031889.
XX PR 08-JUN-2001; 2001KRR-00031889.
XX PA (SAMY-) SANYANG GENEX CORP.

XX PT Gene expression system useful for mass-production of peptide antibiotics.
PT and vectors derived from microorganisms.
XX DR WPI; 2002-301977/34.
XX P-PSDB; ABBB1940.
XX Disclosure; Page 17; 56pp; Korean.

XX The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purF gene or its derivative, and a second gene sequence which codes

peptide antibiotics. The mass-production method of peptide antibiotics comprises the steps of: constructing an expression vector including the genetic component, transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of pGKX2, pGKX4 and pGKX5, and it has a high copy number of origin, strong transcription promoter and structural gene. The sequences given in records ABL60400-ABL60464 represent DNA sequences of the invention

XX Sequence 53 3P, 8 A; 12 C; 20 G; 13 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.267 Length: 53
 Score: 73.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 80.22% Indels: 0
 DB: 6 Gaps: 0

US-09-444-281-35 (1-13) x ABL60445 (1-53)

QY 4 LysTrpProTrpTrpProTrpArg 12
 Db 17 AAATGCCGTGGCCGTGGCTGCGTGTG 43

RESULT 13

AAI72481
 ID AAI72481 standard; cDNA; 68 BP.
 XX
 AC AAI72481;
 XX
 DT 16-MAY-2002 (first entry)

DE cDNA derived from C-terminus of ubiquitin.

XX Recursive ensemble mutagenesis; REM; cell viability; optical signal; high-throughput screening; antimicrobial compound; antibiotic; ss.
 KW
 KW
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT CDS 1. .60
 FT /*tag= a
 FT /transl_except= pos:28..30,aa:Trp
 FT /partial
 FT /note= "No start codon given"
 PN WC200206517-A2.
 XX
 PD 24-JAN-2002.
 PF 19-JUL-2001; 2001WO-US023004.
 XX
 PR 19-JUL-2000; 2000US-0219179P.
 XX
 PA (KAIROS SCI INC.,
 XX
 PI Bylina EJ, Coleman WJ, Youyan DC;
 XX
 DR WPI: 2002-179801/23.
 DR P-PSDB; AAB47907.

XX Screening compounds affecting cell viability e.g. for identifying antimicrobial compounds, comprises determining if induced transformed cell colonies have a desired signal when contacted with a viability indicator.
 XX Disclosure; Fig 6; 56PP; English.
 XX This sequence is derived from the C-terminus of ubiquitin and represents the cloning region. SacII-BglII cassettes can be used for inserting antimicrobial peptide sequences into this region. This sequence may be
 PS
 XX
 CC
 CC

used to form the recursive ensemble mutagenesis (REM) cassette of the invention. The cassette may be used in the method of the invention for determining whether a compound affects cell viability by: (a) exposing colonies of cells (CC) on a support surface to inducing conditions, where the cells have been transformed with an expression library encoding candidate compounds; (b) contacting CC with a viability indicator that produces an optical signal indicative of cell viability; and (c) determining if a colony has a desired optical signal. The method is useful for determining whether a compound affects cell viability. It is useful for high-throughput screening to identify antimicrobial compounds and in drug discovery. The antimicrobial compounds are useful in the pharmaceutical industry, and provide an additional new class of antibiotic compounds to fight infectious diseases. The method is useful for assaying the authentic peptide sequences contained in an expression library for antimicrobial activity, for distinguishing dead cells (expressing active sequences) from living cells (expressing inactive or less active sequences), to identify novel antimicrobial peptide sequences, including highly potent molecules, resulting in a large number of new antimicrobial lead compounds that are active against a broad range of bacteria or other microorganisms, and for screening all types of antibiotic compounds, including libraries of molecules produced by metabolic engineering and artificial synthesized CC molecules in solid-phase arrays

XX Sequence 68 BP; 11 A; 18 C; 19 G; 20 T; 0 U; 0 Other;

SQ

Alignment Scores:
 Pred. No.: 0.349 Length: 68
 Score: 73.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 80.22% Indels: 0
 DB: 6 Gaps: 0

US-09-444-281-35 (1-13) x AAI72481 (1-68)

QY 4 LysTrpProTrpTrpProTrpArg 12
 Db 31 AAATGCCGTGGCCGTGGCTGCGTGC 57

RESULT 14

AAZ40246
 ID AAZ40246 standard; DNA; 69 BP.
 XX
 AC AAZ40246;
 XX
 DT 23-FEB-2000 (first entry)

XX Oligonucleotide for cloning indolicidin peptide coding sequence.
 KW Indolicidin; bactenecin; sulphate-reducing bacteria; growth inhibitor; KW corrosion; degradation; metal; concrete; cement; dental implant; biofilm; KW ss.
 XX Synthetic.
 OS Bacillus sp.
 XX PN WO95553-A1.
 XX PD 11-NOV-1999.
 XX PF 03-MAY-1999; 99WO-US009675.
 XX PR 06-MAY-1998; 98US-00074037.
 PR 31-MAR-1999; 99US-00282277.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PI Wood TK, Jayaraman A, Barthman JC;
 XX DR WPI: 2000-052882/04.
 XX Inhibiting growth of sulfate-reducing bacteria using other bacteria,
 PT

PT particularly for protection of metals and concrete.
 XX Example 4; Fig 1; 84pp; English.
 PS This sequence represents an oligonucleotide for cloning the non-amidated indolicidin peptide coding sequence. The invention relates to a method for inhibiting growth of sulphate-reducing bacteria (A) on a material (B) sensitive to corrosion or degradation, by applying to (B) a bacterium (C) that secretes a compound (1) able to inhibit growth of (A). The method is used to protect metal, concrete or cement against corrosion and degradation, but (B) can also be used to protect dental implants, (B) is present in an open or closed system (e.g. water cooling tower, liquid storage container, fuel tank, sewer or drainage system etc.) or part of a bridge or other structure. The method is more effective and less expensive than known methods for inhibiting (A), and reduces the amount of toxic chemicals released. Conventional biofilms of aerobic organisms tends to encourage growth of (A), and addition of (C) to the biofilm prevents this. A single application of (C) lasts for a long time, and (1) are produced exactly where they are required and inhibit (A) without significant impact on other organisms (this effect includes reducing resistance of (A) to conventional biocides, which may then be used in reduced amounts). If local damage to the biofilm occurs, the underlying material is still protected by diffusion of (1) from neighbouring areas
 XX Sequence 69 BP; 14 A; 18 C; 20 G; 17 T; 0 U; 0 Other;
 SQ

Alignment Scores:

Pred. No. : 0.355 Length: 69
 Score: 73.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 80.22% Indels: 0
 DB: 3 Gaps: 0

US-09-444-281-35 (1-13) x AA240246 (1-69)

QY 4 LysTrpProTrpTrpTrpTrpTrpTrpArgArg 12
 Db 28 AAATGGCCCTGGCTGGCGCGCGC 54

RESULT 15

AA249764 standard; DNA; 211 BP.
 ID AA249764
 AC AA249764;

XX DT 18-APR-2000 (first entry)

XX Poly-(Indol (1-13)-Met-Ala-Arg-Ile-Ala-Met)3 DNA.

XX Crosslinked indolicidin analog; X-indolicidin; poly-Indol 1-13; stability; bovine neutrophil; antimicrobial; antibacterial; fungicide; protozoacide; virus; anti-HIV; human immunodeficiency virus-1; HIV-1; gram positive bacteria; gram negative; Staphylococcus aureus; Escherichia coli; Salmonella typhimurium; yeast; fungi; protozoa; Candida albicans; Cryptococcus neoformans; Giardia; Acanthamoeba; hexapeptide spacer; ds.

XX Synthet. 1-21 b

OS Bos sp.

XX FH Key

FT primer_bind 8.199

FT CDS /*tag= a

FT /*tag= "Poly-(Indol (1-13)-Met-Ala-Arg-Ile-Ala-Met)3"
 FT /product= "Poly-(Indol (1-13)-Met-Ala-Arg-Ile-Ala-Met)3"
 FT /note= "encodes three copies of Indol 1-13, each separated by Met-Ala-Arg-Ile-Ala-Met spacer sequence"
 FT misc_feature 68 .71 /*tag= d
 FT /note= "corresponds to overlap in oligonucleotides used for ligation"

FT misc_feature 148.151 /*tag= e
 FT /note= "corresponds to overlap in oligonucleotides used for ligation"
 FT primer_bind
 FT XX complement (191. 211)
 FT XX /*tag= c
 FT XX W0996510-A1.
 FT XX PD 23-DEC-1999.
 FT XX PF 20-MAY-1999;
 FT XX PR 18-JUN-1998;
 FT XX (REBC) UNIV CALIFORNIA.
 FT XX Selsted ME, Osapay K;
 FT XX WPI: 2000-147133/13.
 FT DR P-PSDB; AA44668.
 FT XX Crosslinked indolicidin analogs with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.
 FT XX PS Example 1C; Fig 1; 53pp; English.
 FT XX
 CC The patent discloses crosslinked analogs of indolicidin (Indol 1-13) which is a naturally occurring peptide isolated from bovine neutrophils and has antimicrobial activity. The crosslinked indolicidin (X-indolicidin) analogs are stable and have antimicrobial activity against gram positive and negative bacteria (e.g. Staphylococcus aureus, Escherichia coli and Salmonella typhimurium), yeasts and fungi (e.g. Candida albicans, Cryptococcus neoformans), protozoa (e.g. Giardia species and Acanthamoeba species), and viruses (e.g. HIV-1). They can be used for reducing or inhibiting the growth or survival of microorganisms in an environment e.g. a food or food product, a solution, an inanimate object comprising a surface, or a mammal. The present sequence is a DNA encoding a protein comprising three copies of Indol 1-13 each separated by a hexapeptide spacer sequence. The sequence was used to produce a recombinant construct for the expression of Indol-homoserine (Hse) analog. The ability of Indol-Hse analog to maintain antimicrobial activity provides a means to produce X-indolicidin analog precursors in sufficient quantities

XX SQ Sequence 211 BP; 36 A; 50 C; 74 G; 51 T; 0 U; 0 Other;
 XX Alignment Scores:
 CC Pred. No. : 1.18 Length: 211
 CC Score: 73.00 Matches: 9
 CC Percent Similarity: 100.00% Conservative: 0
 CC Best Local Similarity: 100.00% Mismatches: 0
 CC Query Match: 80.22% Indels: 0
 CC DB: 3 Gaps: 0
 CC US-09-444-281-35 (1-13) x AA249764 (1-211)
 CC QY 4 LysTrpProTrpTrpTrpTrpTrpTrpTrpArgArg 12
 CC Db 38 AAATGGCCCTGGCTGGCGCGC 64

CC Search completed: May 11, 2004, 14:43:51
 CC Job time : 260.88 secs

is the number of results predicted by chance to have a score higher than or equal to the score of the result being printed, derived by analysis of the total score distribution.

SUMMARIES			
Query	Match	Length	DB ID
1	Issued_Parents_NA_*	1	
2	/cgn2_6/podata/2/ina/5A_COMB_seq:*	1	
3	/cgn2_6/podata/2/ina/5B_COMB_seq:*	1	
4	/cgn2_6/podata/2/ina/6A_COMB_seq:*	1	
5	/cgn2_6/podata/2/ina/6B_COMB_seq:*	1	
6	/cgn2_6/podata/2/ina/backfiles1.seq:*	1	

4

5

Start	End	Matrix	Length	DB	ID	Description
1	100	-END=1	MATRIX-X=0	DB=62	-TRANS-human40	cdi
2	100	-TIR SCORE=100	-TIR MAX=100	-TIR MIN=0	-ALIGN=15	
3	100	-NORM=EXT	-NORM=EXT	-NORM=EXT	-MAXLEN=0	-MAXLEN=2000000000
4	100	-PROT=PRO	-PROT=PRO	-PROT=PRO	-ICPU=3	
5	100	-WAIT=0.5	-WAIT=0.5	-WAIT=0.5	-LONGLOG	
6	100	-XGAP=0.5	-XGAP=0.5	-XGAP=0.5	-XGAPEXT=0.5	-XGAP=0.5
7	100	-DELEXT=7	-DELEXT=7	-DELEXT=7	-DELEXT=7	

Result No.	Pred. No.	Score
1	91	score green
2	73	and is de-
3	73	ferred
4	73	is de-
5	73	ferred
6	6	is de-
7	73	ferred
8	73	is de-
9	63	ferred
10	63	is de-
11	63	ferred
12	12	is de-

LENGTH: 88 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLogy: linear
 US-09-042-071-49

Alignment Scores:
 Pred. No.: 0.00168
 Score: 91.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 3

US-09-444-281-35 (1-13) x US-09-042-071-49 (1-88)

QY 1 IleLeuIysLysTrpProTrpProTrpProTrpArgArgys 13
 Db 25 ATCTGAAAATGGCGTGGCGCTGGCGTGGCTGATAA 63

RESULT 2
 US-09-042-071-49
 ; Sequence 29, Application US/09230180
 ; Patent No. 6183392
 ; GENERAL INFORMATION:
 ; APPLICANT: Kim, Sun-Chang
 ; APPLICANT: Lee, Jie Hyun
 ; APPLICANT: Kang, Min Hyung
 ; APPLICANT: Kim, Jeong Hyun
 ; APPLICANT: Hong, Seung-Suh
 ; APPLICANT: Lee, Hyun-Soo
 ; APPLICANT: Samsung Genex Corporation
 ; TITLE OF INVENTION: METHOD FOR MASS PRODUCTION OF
 ; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE
 ; FILE REFERENCE: 6181/0F135
 ; CURRENT APPLICATION NUMBER: US/09/230,180
 ; CURRENT FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: PCT/KR98/00132
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: KR 13372/1998
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: KR 21312/1997
 ; PRIOR FILING DATE: 1997-05-28
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 29
 ; LENGTH: 39
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: DNA sequence deduced from Indolicidin peptide
 ; OTHER INFORMATION: sequence based on codon usage of *E. coli*
 US-09-230-180-29

Alignment Scores:
 Pred. No.: 0.0847
 Score: 73.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 80.22%
 DB: 3

US-09-444-281-35 (1-13) x US-09-230-180-29 (1-39)

QY 4 LysTrpProTrpProTrpProTrpArgArg 12
 Db 13 ATGGCCGTGGCTGGCGTGGCTGCTG 39

RESULT 3
 US-09-282-277-1
 ; Sequence 1, Application US/09282277
 ; Patent No. 6630197

Alignment Scores:
 Pred. No.: 0.153
 Score: 73.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 80.22%
 DB: 4

US-09-444-281-35 (1-13) x US-09-282-277-1 (1-211)

QY 4 LysTrpProTrpProTrpProTrpArgArg 12

Db 38 AAATGCCCTGGGGCGTCGT 64
 RESULT 5
 US-09-416-481A-38
 Sequence 38, Application US/09416481A
 / Patent No. 652455
 / GENERAL INFORMATION:
 / APPLICANT: Selsick, Michael E.
 / TITLE OF INVENTION: Indolicidin Analogs and Methods of Using Same
 / FILE REFERENCE: P-UC 3794
 / CURRENT APPLICATION NUMBER: US/09/416, 481A
 / PRIORITY NUMBER: US 09/076, 227
 / PRIORITY FILING DATE: 1998-05-12
 / NUMBER OF SEQ ID NOS: 39
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO: 38
 / LENGTH: 211
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (8) .. (196)
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 / OTHER INFORMATION: construct
 US-09-416-481A-38

Alignment Scores:
 Pred. No.: 0.491 Length: 211
 Score: 73.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 80.22% Indels: 0
 DB: 4

US-09-444-281-35 (1-13) x US-09-416-481A-38 (1-211)

QY 4 LysTrpProTrpProTrpArg 12
 Db 38 AAATGCCCTGGGGCGTCGT 64
 RESULT 6
 US-09-259-741-5
 Sequence 5, Application US/09259741
 / Patent No. 6033895
 / GENERAL INFORMATION:
 / APPLICANT: GARGER, STEPHEN
 / APPLICANT: HOLTZ, R. BARRY
 / APPLICANT: MCCULLOCH, MICHAEL
 / APPLICANT: TURPEN, THOMAS
 / TITLE OF INVENTION: A PROCESS FOR ISOLATING AND PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT SOURCES
 / TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT SOURCES
 / NUMBER OF SEQUENCES: 5
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Howrey & Simon
 / STREET: 1299 Pennsylvania Avenue N.W.
 / CITY: Washington
 / STATE: DC
 / ZIP: 20004
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: DOS
 / SOFTWARE: FASTSEQ for Windows Version 2.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/259, 741
 / FILING DATE: February 25, 1999
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 09/037, 751

SEQUENCE CHARACTERISTICS:
 LENGTH: 6446 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Genomic RNA
 US-09-437-751-5

Alignment Scores:
 Pred. No.: 17.2 Length: 6446
 Score: 73.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 80.22% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-35 (1-13) x US-09-466-422-5 (1-6446)

QY 4 LysTrpProTrpTrpProTrpArgArg 12
 Db 6213 AAUGGCCUUGGGCAUUGGCAGGCGCA 6239

RESULT 9
 US-09-252-991A-9269 (1-6446)
 QY 4 LysTrpProTrpTrpProTrpArgArg 12
 Db 6213 AAUGGCCUUGGGCAUUGGCAGGCGCA 6239

RESULT 9
 US-09-252-991A-9269 (1-6446)
 QY 4 LysTrpProTrpTrpProTrpArgArg 12
 Db 6213 AAUGGCCUUGGGCAUUGGCAGGCGCA 6239

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074, 788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094, 190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 9269
 LENGTH: 1278
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9269 (1-6446)

Alignment Scores:
 Pred. No.: 45.3 Length: 1278
 Score: 63.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 69.23% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-35 (1-13) x US-09-252-991A-9269 (1-1278)

QY 5 TrpProTrpTrpProTrpArg 11
 Db 885 TGCCTCTGGCGCCCTGGCA 905

RESULT 10
 US-09-252-991A-9298/C (1-1278)
 QY 5 TrpProTrpTrpProTrpArg 11
 Db 885 TGCCTCTGGCGCCCTGGCA 905

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074, 788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094, 190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 9298
 LENGTH: 1362
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-9298 (1-1278)

Alignment Scores:
 Pred. No.: 48.4 Length: 1362

US-08-481-337A-1
 ; Sequence 1, Application US/08481337A
 ; GENERAL INFORMATION:
 ; Patent No. 5863738
 ; APPLICANT: TEN DLUKE, Peter
 ; APPLICANT: HELDIN, Carl-Henrik
 ; APPLICANT: MIYAZONO, Kohji
 ; APPLICANT: SAMPATH, Kuber T.
 ; TITLE OF INVENTION: Morphogenic Protein-Specific Cell
 ; TITLE OF INVENTION: Surface Receptors and Uses Therefor
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Testa, Hurwitz & Thibeault
 ; STREET: 125 High St.
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110
 ; COMPUTER READABLE FORM:
 ; COMPUTER: IBM PC compatible
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/481,337A
 ; FILING DATE: 02-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MEYERS, Thomas C.
 ; REGISTRATION NUMBER: 36,989
 ; REFERENCE/DOCKET NUMBER: CRP-097CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 248-7000
 ; TELEFAX: (617) 248-7100
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1509 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1509
 ; OTHER INFORMATION: /product= "Human ALK-1"
 ; US-08-481-337A-1

Alignment Scores:
 Pred. No.: 203 Length: 1509
 Score: 58.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 63.74% Indels: 0
 DB: 2 Gaps: 0

US-09-444-281-35 (1-13) x US-08-696-268B-1 (1-1509)

Qy 5 TrpProTrpTrpProTrp 10
 Db 389 TGGCCCTGATGGCTCTGG 406

RESULT 15
 US-08-696-268B-1
 ; Sequence 1, Application US/08696268B
 ; Patent No. 5868752
 ; GENERAL INFORMATION:
 ; APPLICANT: ICHIGO, HIDENORI
 ; APPLICANT: NISHITOH, HIDEKI
 ; APPLICANT: SAMPATH, KUBER T.
 ; TITLE OF INVENTION: NOVEL SIGNALLING RECEPTOR FOR
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:

Copyright (c) 1993 - 2004 Compugen Ltd.	Gencore version 5.1.6
Run on:	May 11, 2004, 14:35:33 ; Search time 281.32 Seconds (without alignments)
	209.334 Million cell updates/sec
Title:	US-09-444-281-35
Sequence:	1 IILKWPWPKWPK 13
Scoring table:	BLOSUM62
	Xgapop 10.0 , Xgapext 0.5
	Ygapop 10.0 , Ygapext 0.5
	Fgapop 6.0 , Fgapext 7.0
	Delop 6.0 , Delext 7.0
Searched:	2941586 seqs, 2264995651 residues
Total number of hits satisfying chosen parameters:	
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing: Minimum Match 0% Maximum Match 100% Tiling: First 45 summaries	

Sequence 132877,

ALIGNMENTS

RESULT 1

US-10-395-896-32

Sequence 32, Application US/10395896

Publication No. US20030219054A1

GENERAL INFORMATION:

APPLICANT: Guarna, Maria Marta

APPLICANT: Chen, Yuchen

APPLICANT: Cory, Robert

APPLICANT: Brinkman, Jacqui

APPLICANT: Cabralda, Jennifer

APPLICANT: Metlitskaya, Lubna

APPLICANT: Suleman, Dinar

TITLE OF INVENTION: METHODS FOR PRODUCING MC

TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES

FILE REFERENCE: 660081-421

CURRENT APPLICATION NUMBER: US/10/395,896

CURRENT FILING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSeq For Windows Version 4.0

SEQ ID NO 32

LENGTH: 72

TYPE: DNA

ORGANISM: Artificial Sequence

1	76	83.5	72	16	US-10-395-896-32	Sequence 32, App1
2	76	83.5	139	16	US-10-395-896-31	Sequence 31, App1
3	75	82.4	121	16	US-10-395-896-28	Sequence 28, App1
4	75	82.4	121	16	US-10-395-896-62	Sequence 62, App1
5	75	82.4	123	16	US-10-395-896-29	Sequence 29, App1
6	75	82.4	166	16	US-10-395-896-30	Sequence 30, App1
7	73	80.2	68	9	US-09-309-552-6	Sequence 6, App1
8	73	80.2	550	15	US-10-076-816-60	Sequence 60, App1
9	73	80.2	6446	15	US-09-962-527-5	Sequence 5, App1
10	70	76.9	114	16	US-10-395-896-64	Sequence 64, App1
11	70	76.9	114	16	US-10-395-896-65	Sequence 65, App1
12	66	72.5	207	15	US-10-252-773-2	Sequence 25, App1
13	64	70.3	39	15	US-10-252-773-15	Sequence 15, App1
14	64	70.3	53	15	US-10-252-773-17	Sequence 17, App1
15	64	70.3	54	15	US-10-252-773-19	Sequence 19, App1
16	64	70.3	557	13	US-10-027-632-53929	Sequence 53929, A
17	64	70.3	557	13	US-10-027-632-321717	Sequence 321717, A
18	64	70.3	557	16	US-10-027-632-33929	Sequence 53929, A
19	64	70.3	557	16	US-10-027-632-321717	Sequence 321717, A
20	63	69.2	122	9	US-09-783-590-1444	Sequence 1444, AP
21	63	69.2	1437	9	US-09-815-542-7766	Sequence 7766, AP
22	63	69.2	1908	9	US-09-815-542-9716	Sequence 9716, AP
23	63	69.2	1908	13	US-10-282-112A-39517	Sequence 39517, A
24	61.5	67.6	571	13	US-10-025-114-14181	Sequence 1181, A
25	60	65.9	577	15	US-10-029-386-12845	Sequence 12845, A
26	60	65.9	1526	13	US-10-424-591-17644	Sequence 17644, A
27	60	65.9	2403	15	US-10-156-761-1600	Sequence 1600, AP
28	60	65.9	14739	15	US-10-017-161-1557	Sequence 1557, AP
29	60	65.9	14739	16	US-10-292-118-1245	Sequence 1245, AP
30	60	65.9	34570	12	US-09-397-72-157	Sequence 157, APP
31	60	65.9	902608	15	US-10-156-761-1	Sequence 1, App1
32	59.5	65.4	1224	16	US-10-369-493-40678	Sequence 40678, A
33	59	64.8	502	13	US-10-027-532-44536	Sequence 44536, A
34	59	64.8	502	16	US-10-027-532-44536	Sequence 44536, A
35	59	64.8	627	13	US-10-027-632-94574	Sequence 94574, A
36	59	64.8	627	16	US-10-027-632-94574	Sequence 94574, A
37	59	64.8	669	16	US-10-260-238-59	Sequence 17642, A
38	59	64.8	837	13	US-10-424-591-17642	Sequence 17642, A
39	59	64.8	1825	16	US-10-116-275-21	Sequence 275, AP
40	59	64.8	2218	10	US-09-020-790-1	Sequence 1, App1
41	58	63.7	228	11	US-09-923-876-3798	Sequence 3798, AP
42	58	63.7	63.7	9	US-09-923-876-3798	Sequence 3798, AP
43	58	63.7	429	13	US-10-424-591-1131	Sequence 1131, AP
44	58	63.7	496	13	US-10-424-591-92875	Sequence 92875, A
45	58	63.7	767	13	US-10-027-632-132877	Sequence 132877, A

GENERAL INFORMATION:

APPLICANT: Guarra, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
APPLICANT: Brinkman, Jacqui
APPLICANT: Cabralda, Jennifer
APPLICANT: Metlitskia, Lubna
APPLICANT: Suleman, Dinar

TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED PEPTIDES

FILE REFERENCE: 660081-421

CURRENT APPLICATION NUMBER: US/10/395, 896

CURRENT FILING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 29

LENGTH: 123

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Exemplary "template"

US-10-395-896-29

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
	0.131	123	9	1	100.00%	90.00%	82.42%	16

US-09-444-281-35 (1-13) x US-10-395-896-29 (1-123)

Qy 4 LysTrpProTrpTrpProTrpArgArgLys 13
Db 32 CTTGGCCGGTGGTGGCGGTGCGTCGCAA 61

RESULT 6

US-10-395-896-30

Sequence 30, Application US/10395896

GENERAL INFORMATION:

APPLICANT: Guarra, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
APPLICANT: Brinkman, Jacqui
APPLICANT: Cabralda, Jennifer
APPLICANT: Metlitskia, Lubna
APPLICANT: Suleman, Dinar

TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED PEPTIDES

FILE REFERENCE: 660081-421

CURRENT APPLICATION NUMBER: US/10/395, 896

CURRENT FILING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 166

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Exemplary "template"

US-10-395-896-30

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
	0.173	166	9	1	100.00%	90.00%	82.42%	16

US-09-444-281-35 (1-13) x US-10-395-896-30 (1-166)

Qy 4 LysTrpProTrpTrpProTrpArgArgLys 13
Db 25 CGTGGCCGTGGTGGCCGTCGCAA 54

RESULT 7

US-09-909-652-6

Sequence 6, Application US/09909652

GENERAL INFORMATION:

Patent No. US20020025537A1

APPLICANT: Kairos Scientific, Inc.
APPLICANT: Bylina, Edward J.
APPLICANT: Colemai, William J.
APPLICANT: Youvan, Douglas C.

TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING A LIBRARY OF INVENTION: AND SCREENING COMPOUNDS THAT AFFECT CELL VIABILITY

FILE REFERENCE: 22346-7001

CURRENT APPLICATION NUMBER: US/09/909, 652

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US 60/219, 179

PRIOR FILING DATE: 2000-07-19

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 68

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Nucleic acid encoding ubiquitin indolicidin fusion protein fragment

US-09-909-652-6

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
	0.133	68	9	1	100.00%	100.00%	80.22%	9

US-09-444-281-35 (1-13) x US-09-909-652-6 (1-68)

Qy 4 LysTrpProTrpTrpProTrpArgArgLys 12
Db 31 AAATGGCCCTGGTGGCGTCGCGC 57

RESULT 8

US-10-076-816-60

Sequence 60, Application US/10076816

GENERAL INFORMATION:

Publication No. US2003056244A1

APPLICANT: Huang, Ning
APPLICANT: Rodriguez, Raymond
APPLICANT: Hagle, Frank E.

TITLE OF INVENTION: Feed Additive Compositions and Methods

FILE REFERENCE: 5065-8021-US00

CURRENT APPLICATION NUMBER: US/10/076, 816

PRIOR APPLICATION NUMBER: 2002-02-14

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: US 60/269, 188

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 09/847, 232

PRIOR FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: US 60/246, 929

PRIOR FILING DATE: 2001-02-06

PRIOR APPLICATION NUMBER: US 60/201, 182

PRIOR FILING DATE: 2003-05-02

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 60

LENGTH: 550

TYPE: DNA

ORGANISM: Bos taurus

US-10-076-816-60

Alignment Scores:
 Pred. No.: 0.953
 Score: 73.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 80.22%
 DB: 15

Length: 550
 Matches: 9
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-444-281-35 (1-13) x US-10-076-816-60 (1-550)

QY 4 LysTrpProTrpTrpProTrpArgArg 12
 Db 415 AATGGCCTGGCCAUAGGCGCA 441

RESULT 9
 US-09-062-527-5
 ; Sequence 5, Application US/09962527
 ; Publication No. US2003049813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GARGER, STEPHEN
 ; HOLTZ, R. BARRY
 ; MCCULLOCH, MICHAEL
 ; TURPEN, THOMAS
 ; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT SOURCES
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howrey & Simon
 ; STREET: 1299 Pennsylvania Avenue N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/962,527
 ; FILING DATE: 24-Sep-2001
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 09/037,751
 ; FILING DATE: 10-march-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Halluin, Albert P
 ; REGISTRATION NUMBER: 25,277
 ; REFERENCE/DOCKET NUMBER: 00601.0140.999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-463-8109
 ; TELEFAX: 650-463-8400
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6446 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: Genomic RNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 ; US-09-962-527-5

Alignment Scores:
 Pred. No.: 9.69
 Score: 73.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 80.22%
 DB: 10

Length: 6446
 Matches: 9
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-444-281-35 (1-13) x US-09-962-527-5 (1-6446)

QY 4 LysTrpProTrpTrpProTrpArgArg 12
 Db 6213 AAGGGCTTGGCCAUAGGCGCA 6239

RESULT 10
 US-10-395-895-64
 ; Sequence 64, Application US/10395896
 ; Publication No. US20030219854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarna, Maria Marta
 ; APPLICANT: Chen, Yuchen
 ; APPLICANT: Cory, Robert
 ; APPLICANT: Brinkman, Jacqui
 ; APPLICANT: Cabralda, Jennifer
 ; APPLICANT: Matiliskala, Luba
 ; APPLICANT: Suleiman, Dinar
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES
 ; FILE REFERENCE: 660081-421
 ; CURRENT APPLICATION NUMBER: US/10/395,896
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 64
 ; LENGTH: 114
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Nucleic acid template encoding precursor peptide S21.
 ; OTHER INFORMATION: 11B25 and anionic spacer peptide S21.
 ; US-10-395-895-64

Alignment Scores:
 Pred. No.: 0.513
 Score: 70.00
 Percent Similarity: 100.00%
 Best Local Similarity: 88.89%
 Query Match: 76.92%
 DB: 16
 ; LENGTH: 114
 ; Matches: 8
 ; Conservat: 1
 ; Mismatches: 0
 ; Indels: 0
 ; Gaps: 0

US-09-444-281-35 (1-13) x US-10-395-895-64 (1-114)

QY 4 LysTrpProTrpTrpProTrpArgArg 12
 Db 36 CGTTGGCCGCTGGCCCTGGCTGGCTGC 62

RESULT 11
 US-10-395-895-65/C
 ; Sequence 65, Application US/10395896
 ; Publication No. US20030219854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarna, Maria Marta
 ; APPLICANT: Chen, Yuchen
 ; APPLICANT: Cory, Robert
 ; APPLICANT: Brinkman, Jacqui
 ; APPLICANT: Cabralda, Jennifer
 ; APPLICANT: Matiliskala, Luba
 ; APPLICANT: Suleiman, Dinar
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES
 ; FILE REFERENCE: 660081-421
 ; CURRENT APPLICATION NUMBER: US/10/395,896
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 65
 ; LENGTH: 114
 ; Matches: 7
 ; Conservat: 1
 ; Mismatches: 0
 ; Indels: 0
 ; Gaps: 0

US-09-444-281-35 (1-13) x US-10-395-895-64 (1-114)

QY 4 LysTrpProTrpTrpProTrpArgArg 12
 Db 36 CGTTGGCCGCTGGCCCTGGCTGGCTGC 62

OTHER INFORMATION: 11B25 and anionic spacer peptide S21.
US-10-395-896-65

Alignment Scores:
Pred. No.: 0.513 Length: 114
Score: 70.00 Matches: 8
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 76.92% Indels: 0
DB: 16 Gaps: 0

US-09-444-281-35 (1-13) x US-10-395-896-65 (1-114)

Qy 4 LysTrpProTrpProTrpArg12
Db 79 CTTGGCCGTCGTCGCGCGC 53

RESULT 12
US-10-252-773-25
; Sequence 25, Application US/10252773
; Publication No. US20030131383A1
; GENERAL INFORMATION:
; APPLICANT: EVERETT, NICHOLAS P.
; APPLICANT: LI, QUNIGSHUN
; APPLICANT: LAWRENCE, CHRISTOPHER
; APPLICANT: DAVIES, MAELOR H.
; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
; TITLE OF INVENTION: DEGRADATION
; FILE REFERENCE: INTERLINK 3.0-003
; CURRENT APPLICATION NUMBER: US/10/252,773
; PRIORITY FILING DATE: 2002-09-23
; PRIORITY FILING DATE: 1998-10-30
; PRIORITY FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA PCRIL
; OTHER INFORMATION: construct
US-10-252-773-25

Alignment Scores:
Pred. No.: 2.85 Length: 207
Score: 66.00 Matches: 6
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 60.00% Mismatches: 0
Query Match: 72.53% Indels: 0
DB: 15 Gaps: 0

US-09-444-281-35 (1-13) x US-10-252-773-25 (1-207)

Qy 2 LeuLysTrpProTrpProTrpArg11
Db 163 ATTAAGGAGATGGCTTGTGGCTTGGAA 192

RESULT 13
US-10-252-773-15
; Sequence 15, Application US/10252773
; Publication No. US20030131383A1
; GENERAL INFORMATION:
; APPLICANT: EVERETT, NICHOLAS P.
; APPLICANT: LI, QUNIGSHUN
; APPLICANT: LAWRENCE, CHRISTOPHER
; APPLICANT: DAVIES, MAELOR H.
; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
; TITLE OF INVENTION: DEGRADATION
; FILE REFERENCE: INTERLINK 3.0-003

OTHER INFORMATION: Description of Artificial Sequence:
US-10-252-773-15

Alignment Scores:
Pred. No.: 1.05 Length: 39
Score: 64.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 70.33% Indels: 0
DB: 15 Gaps: 0

US-09-444-281-35 (1-13) x US-10-252-773-15 (1-39)

Qy 3 LysLysTrpProTrpProTrpArg11
Db 1 AGGAGATGGCTTGTGGCTTGGAA 27

RESULT 14
US-10-252-773-17/C
; Sequence 17, Application US/10252773
; Publication No. US20030131383A1
; GENERAL INFORMATION:
; APPLICANT: EVERETT, NICHOLAS P.
; APPLICANT: LI, QUNIGSHUN
; APPLICANT: LAWRENCE, CHRISTOPHER
; APPLICANT: DAVIES, MAELOR H.
; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
; TITLE OF INVENTION: DEGRADATION
; FILE REFERENCE: INTERLINK 3.0-003

CURRENT APPLICATION NUMBER: US/10/252,773
; CURRENT FILING DATE: 2002-09-23
; PRIORITY FILING DATE: 1998-10-30
; PRIORITY FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-252-773-17

Alignment Scores:
Pred. No.: 1.4 Length: 53
Score: 64.00 Matches: 6
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 66.67% Mismatches: 0
Query Match: 70.33% Indels: 0
DB: 15 Gaps: 0

US-09-444-281-35 (1-13) x US-10-252-773-17 (1-53)

Qy 3 LysLysTrpProTrpProTrpArg11
Db 53 AGGAGATGGCTTGTGGCTTGGAA 27

RESULT 15

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 11, 2004, 14:00:48 ; Search time 1721.2 Seconds

(without alignments)
225.545 Million cell updates/sec

Title: US-09-444-281-35
Perfect score: 91
Sequence: 1_LIKKNPWWPWRK 13

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delecp 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+P2n,model -DEV=xch
-Q=qm2.1/DSPTO.spoof -SUFFIX=first -MINNAT=CH-0.1 -LOOPENT=0
-DB=EST -QFMT=fastap -SUFFIX=first -MINNAT=CH-0.1 -LOOPENT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40_cdi -LFRST=45
-DOCALIGNN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGNN=15 -NODE=LOCAL
-OUTTYPE=txt -NORM=ext -HEAPSIZE=500 -MINLEN=20000000000
-USER=US09444281 @CCN 1.1 3596 @runat 07052004 171138 2579 -NCPU=6 -ICPU=3
-NO_NMAP -LARGEQUERY -NEG_SCORE=pct -WAIT=0 -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: em_estba:
2: em_estbmu:
3: em_estin:
4: em_estmu:
5: em_estcov:
6: em_estp1:
7: em_estro:
8: em_ntc:
9: gb_est1:
10: gb_est2:
11: gb_htc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estom:
16: em_estom:
17: em_gss_hum:
18: em_gss_pdn:
19: em_gss_rnv:
20: em_gss_vrt:
21: em_gss_fan:
22: em_gss_mam:
23: em_gss_nus:
24: em_gss_pro:
25: em_gss_rnd:
26: em_gss_dhg:
27: em_gss_vrl:
28: gb_gss1:
EST:
RESULT 1
CF479395
LOCUS RTW3_23_A01_51
DEFINITION Well-watered lobolly pine roots RTW3_23_A01_51
ACCESSION CF479395
VERSION CF479395.1
KEYWORDS EST, Pinus taeda (lobolly pine)
SOURCE P. taeda
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus taeda
REFERENCE 1 (bases 1 to 522)

29: gb_gss2:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
1	74	81.3	522	14	CF479395 RTW3_23		
2	70	76.9	263	12	BT976779 485902 MA		
3	69	75.8	330	10	BB024544 89003H02		
c	69	75.8	390	28	AZ218927 RPCI-11-6		
c	69	75.8	757	29	AG185290 Pan trogl.		
c	68	74.7	349	12	BJ476852 BJ476852		
c	7	68	369	12	BJ74341 BJ474341		
c	8	68	381	12	BJ47180 BJ471810		
c	9	68	411	12	BJ47306 BJ473016		
c	10	68	74.7	415	10	BE37369 146629 MA	
c	11	68	74.7	420	9	AV933841 AV933841	
c	12	68	74.7	440	12	BJ471261 BJ471261	
c	13	68	74.7	446	9	AU089922 AU089922	
c	14	68	74.7	446	9	AU198144 AU198144	
c	15	68	74.7	448	9	AU198162 AU198162	
c	16	68	74.7	464	9	AV935002 AV935002	
c	17	68	74.7	471	12	BJ475478 BJ475478	
c	18	68	74.7	472	12	BJ475115 BJ475115	
c	19	68	74.7	472	12	BJ476710 BJ476710	
c	20	68	74.7	473	9	AV937233 AV937233	
c	21	68	74.7	474	12	BJ473880 BJ473880	
c	22	68	74.7	475	9	AU089934 AU089934	
c	23	68	74.7	489	12	BJ477184 BJ477184	
c	24	68	74.7	500	12	BJ475153 BJ475153	
c	25	68	74.7	501	12	BJ470669 BJ470669	
c	26	68	74.7	504	12	BJ475306 BJ475306	
c	27	68	74.7	506	12	BJ471761 BJ471761	
c	28	68	74.7	506	12	BJ473882 BJ473882	
c	29	68	74.7	509	12	BJ471258 BJ471258	
c	30	68	74.7	515	12	BJ469760 BJ469760	
c	31	68	74.7	530	12	BJ472623 BJ472623	
c	32	68	74.7	531	9	BJ475836 BJ475836	
c	33	68	74.7	532	9	AV932159 AV932159	
c	34	68	74.7	539	14	CF346637 JNT1---6-	
c	35	68	74.7	550	14	CF326444 JNT1---6-	
c	36	68	74.7	559	14	CF325873 JNT1---6-	
c	37	68	74.7	578	9	AU082117 AU082117	
c	38	68	74.7	595	14	CF326279 JNT1---6-	
c	39	68	74.7	661	14	CB881162 OSJNNE07B	
c	40	67	73.6	1172	28	BZ552545 pccs1-60-	
c	41	66	72.5	352	9	AU198258 AU198258	
c	42	66	72.5	396	9	AL916683 AL916683	
c	43	66	72.5	434	10	BE453064 BE453064	
c	44	66	72.5	445	12	BG305131 F195a9.Y	
c	45	66	72.5	568	13	CA155445 SCACR2310	

ALIGNMENTS

RESULT 1	CF479395	522 bp	mRNA	linear	EST 08-SEP-2003
LOCUS	RTW3_23_A01_51	Well-watered lobolly pine roots	RTW3	Pinus	
DEFINITION	taed CDNA clone				
ACCESSION	CF479395				
VERSION	CF479395.1				
KEYWORDS	EST, P. taeda (lobolly pine)				
SOURCE	Pinus taeda				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus taeda				
REFERENCE	1 (bases 1 to 522)				

AUTHORS	Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Derrinis, C., Martin, T., White, T., and Neal, D.	JOURNAL	Genome Res. 11 (4), 626-630 (2001)
TITLE	An EST database from well-watered loblolly pine (<i>Pinus taeda</i>) roots	MEDLINE	21180013
JOURNAL	Unpublished (2003)	COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
COMMENT	Other ESTs: RTWMM3_23_A01.bl A022 Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1850 Fax: 706 583 0210 Email: lmp Pratt@uga.edu	DEFINITION	Single pass sequencing. Bases called and alt trimmed with phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. Seq Primer: JENPRAY (CAGCAAAAGCTATGATTCAC).
FEATURES	Location/Qualifiers	PCR PRIMERS	FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTCAGGAGCTATGACCAT Plate: 114 row: F column: 23 Seq Primer: ATTATGGCACATGATG. Location/Qualifiers
FEATURES	Source	Source	organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="pooled" /lab_host="DH10B" /clone lib="MARC 2BOY" /note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue From testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
ORIGIN		Alignment Scores:	Pred. No.: 201 Length: 263 Matches: 8 Conservative: 1 Percent Similarity: 100.00% Best Local Similarity: 88.89% Query Match: 76.92% DB: 126
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	DBPINTION
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	BE024584
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	LOCUS
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	DBPINTION
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	BE024584
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	ACCESSION
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	KEYWORDS
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	SOURCE
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	ORGANISM
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	REFERENCE
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	AUTHORS
ORIGIN		US-09-444-281-35 (1-13) x BI976779 (1-263)	TITLE
REFERENCE	1 (bases 1 to 263)	JOURNAL	Unpublished (2000)
AUTHORS	Smith, T.P.L., Gross, W.M., Franks, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perete, G., Hoit, I., Karanicheva, S., Liang, F., Quackenbush, J. and Keele, J.W.	COMMENT	Contact: Elizabeth H. Harris DCMB Box 91000 Duke University Durham, NC 27708-1000, USA Tel: 919 613 8164 Fax: 919 613 8177 Email: chlamy@duke.edu.
TITLE	Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle	FEATURES	Location/Qualifiers
		Source	1 . 330

```

/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBlueScript II SK+; Site 1: EcoRI; Site 2:
XbaI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XbaI (3') sites.
pBlueScript II SK+ plasmids were excised from the lambda
ZAP clones by superinfection with ExBstI (Stratagene)
phage. The library was normalized using method A described
in Bonaldo et al (1996) Genome Research 6: 791-806."
BRIGITIN

Alignment Scores:
    Scored. No. : 335          Length: 330
    Score: 69.00          Matches: 8
    Percent Similarity: 90.91%  Conservative: 2
    Nearest Local Similarity: 72.73%  Mismatches: 1
    Query Match: 10          Indels: 0
    DB:          Gaps: 0

2005-09-04 11:13:35 (1-13) x BE024584 (1-330)
2Dy 2 LeuLebLysTyrProTrpProTrpProTrpArgArg 12
    66 CITAGAACGGTGGACCTGTCGCGTGGCGCGGG 98

RESULT 4
LOCUS    AZ518927          390 bp  DNA  linear  GSS_16-OCT-2000
DEFINITION RPCI-11-67B18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-67B18,
GENOMIC survey sequence.
ACCESSION AZ518927
VERSION  A0218327.1  GI : 10829921
SOURCE   Homo sapiens (human)
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Butherea; Primates; Catarrhini; Hominidae; Homo.
        1 (bases 1 to 390)
AUTHORS  Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
        Venter,J.C.
TITLE    BAC end sequences of library RPCI-11
JOURNAL  Unpublished (1997)
COMMENT  Other_GSSs: RPCI11-67B18.TU
        Contact: Shaying Zhao
        Department of Eukaryotic Genomics
        The Institute for Genomic Research
        9712 Medical Center Dr., Rockville, MD 20850, USA
        Tel: 301 838 0200
        Fax: 301 838 0208
        Email: szhao@igrap.org
        Clones are derived from the human BAC library RPCI-11. For BAC
        library availability, please contact Pieter de Jong
        (pieter.deJong.med.buffalo.edu). Clones may be purchased from
        BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
        Research Genet CS (info@resgen.com). BAC end search page:
        http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.
        This BAC end was generated during the BAC process and may have
        higher chance of clone tracking errors.
        Seq Primer: T7
        Class: BAC ends.
        Location/Qualifiers
        1. 390
        /organism="Homo sapiens"
FEATURES
    source

```

Score: 69.00
 Percent Similarity: 91.57%
 Best Local Similarity: 83.33%
 Query Match: 75.62%
 DB: 29

US-09-444-281-35 (1-13) x AG185290 (1-757)

Qy 2 LeuIysLysTrpProTrpProTrpProTrpArgLys 13
 Db 279 TTACAAAATCCCCCTGGCCCTGGAGGAG 244

RESULT 6

LOCUS Bj476852 349 bp linear EST 23-MAY-2002

DEFINITION Bj476852 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal137g15 3', mRNA sequence.

ACCESSION Bj476852

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 369)

AUTHORS Sato, K., Saisho, D. and Takeda, K.

JOURNAL Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)

COMMENT Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.

FEATURES source /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Haruna Nijo"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="baal137g15"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 /clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"

ORIGIN

Alignment Scores:
 Pred. No.: 486 Length: 369
 Score: 68.00 Matches: 8
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.73% Indels: 0
 DB: 12 Gaps: 0

US-09-444-281-35 (1-13) x Bj474341 (1-349)

Qy 5 TrpProTrpProTrpProTrpArgArg 12
 Db 275 TGGCCGTGGCCGTGGCGCA 298

RESULT 7

LOCUS Bj474341 369 bp mRNA linear EST 23-MAY-2002

DEFINITION Bj474341 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal137g15 3', mRNA sequence.

ACCESSION Bj474341

VERSION Bj474341.1 GI:21152844

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 369)

AUTHORS Sato, K., Saisho, D. and Takeda, K.

JOURNAL Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)

COMMENT Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.

FEATURES source /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Haruna Nijo"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="baal137g15"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 /clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"

ORIGIN

Alignment Scores:
 Pred. No.: 486 Length: 369
 Score: 68.00 Matches: 8
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.73% Indels: 0
 DB: 12 Gaps: 0

US-09-444-281-35 (1-13) x Bj474341 (1-381)

Qy 5 TrpProTrpProTrpProTrpArgArg 12
 Db 277 TGCCCGTGGCCGTGGCGAGCA 300

RESULT 8

LOCUS Bj471810 381 bp mRNA linear EST 23-MAY-2002

DEFINITION Bj471810 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal21m20 5', mRNA sequence.

ACCESSION Bj471810.1 GI:21150313

VERSION Bj471810.1

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 381)

AUTHORS Sato, K., Saisho, D. and Takeda, K.

JOURNAL Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)

COMMENT Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.

FEATURES source /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Haruna Nijo"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="baal137g15"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 /clone_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"

ORIGIN

Alignment Scores:
 Pred. No.: 455 Length: 349
 Score: 68.00 Matches: 8
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.73% Indels: 0
 DB: 12 Gaps: 0

US-09-444-281-35 (1-13) x Bj476852 (1-349)

Qy 5 TrpProTrpProTrpProTrpArgArg 12
 Db 275 TGGCCGTGGCCGTGGCGCA 298

RESULT 7

LOCUS Bj474341 369 bp mRNA linear EST 23-MAY-2002

DEFINITION Bj474341 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal137g15 3', mRNA sequence.

ACCESSION Bj474341

VERSION Bj474341.1 GI:21152844

/mol_type="mRNA"
 /cultivar="Haruna Nijo"
 /sub_species="vulgaris"
 /db_xref="taxon:112509"
 /clone="baal21m20"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 /clone.lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"
 ORIGIN

Alignment Scores:
 Pred. No.: 505 Length: 381
 Score: 68.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.73% Indels: 0
 DB: 12 Gaps: 0

US-09-444-281-35 (1-13) x BJ473016 (1-381)

Qy 5 TpprotrPrPrPrPrPrPrArg 12
 Db 183 TGCCTGTTGGCTGGCGGA 160

RESULT 9
 BJ473016/c

LOCUS BJ473016 411 bp mRNA linear EST 23-MAY-2002
 DEFINITION Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal40h02 5', mRNA sequence.

VERSION BJ473016.1 GI:21151519
 EST,
 SOURCE Hordeum vulgare subsp. vulgare
 Organism: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
 1 (bases 1 to 411)

REFERENCE Sato, K., Saitoh, D. and Takeda, K.
 AUTHORS Barley EST sequencing project in NIG and Okayama Univ
 TITLE Unpublished (2002)
 JOURNAL
 COMMENT Contact: Tadasu Shin-i
 Center for Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-8856
 Fax: 81-559-81-8855
 Email: cehn@genes.nig.ac.jp.

FEATURES source
 1. .411
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Haruna Nijo"
 /sub_species="vulgaris"
 /db_xref="taxon:112509"
 /tissue_type="top three leaves"
 /dev_stage="adult, heading stage"
 /clone.lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"

ORIGIN

Alignment Scores:
 Pred. No.: 552 Length: 411
 Score: 68.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.73% Indels: 0
 DB: 12 Gaps: 0

US-09-444-281-35 (1-13) x BE237369 (1-415)

Qy 4 LystroPrPrPrPrPrPrArg 11
 Db 280 AAATGCCATGGCCCTGGCGC 303

RESULT 11
 AV933841/C
 LOCUS AV933841 420 bp mRNA linear EST 18-JAN-2002
 DEFINITION AV933841 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,

Qy 5 TpprotrPrPrPrPrPrArg 12
 Db 177 TGGCGTGGTGGCCGTGGCGCA 154

RESULT 10
 BE237369 415 bp mRNA linear EST 25-APR-2001
 Locus BE237369 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.

DEFINITION 146629 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BE237369
 VERSION BE237369.1
 KEYWORDS EST,
 SOURCE Bos taurus (cow)
 ORGANISM Mammalia: Eutheria; Cetartiodactyla; Ruminantia; Peccota; Bovidae; Bovidae; Bos
 Mammalia: Eutheria; Cetartiodactyla; Ruminantia; Peccota; Bovidae; Bovidae; Bos
 REFERENCE 1 (bases 1 to 415)
 Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, F., Wray, J.E., White, J., Cho, J., Fahrkenrug, S.C., Bennett, G.L., Heaton, M.P., Laegrid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, J., Karamycheva, S., Liang, F., Quackenbush, J., and Kele, J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 JOURNAL Genome Res 11 (4), 626-630 (2001)

MEDLINE 21180013
 PUBMED 11282978
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980504.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR PRIMERS
 FORWARD: AGAAACAGCTATGACCAT
 BACKWARD: GTTTTCCAGTACGAGCAG
 Plate: 47 row: J column: 10
 Seq primer: ATTAGTCGACTATAG.

FEATURES source
 1. .415
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DB10B"
 /clone.lib="MARC 4BOV"
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 20 and day 40 embryos."

ORIGIN

Alignment Scores:
 Pred. No.: 559 Length: 415
 Score: 68.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 74.73% Indels: 0
 DB: 10 Gaps: 0

US-09-444-281-35 (1-13) x BE237369 (1-415)

Qy 4 LystroPrPrPrPrPrArg 11
 Db 280 AAATGCCATGGCCCTGGCGC 303

RESULT 11
 AV933841/C
 LOCUS AV933841 420 bp mRNA linear EST 18-JAN-2002
 DEFINITION AV933841 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,

heading stage top three leaves <i>Hordeum vulgare</i> subsp. <i>vulgare</i> cDNA clone <i>baa19005 5'</i> , mRNA sequence.
AV933841 AV933841.1 GI:18229638
EST WORDS EST.
<i>Hordeum vulgare</i> subsp. <i>vulgare</i> <i>Hordeum vulgare</i> subsp. <i>vulgare</i> Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticeae; <i>Hordeum</i> . 1 (bases 1 to 420)
Sato,K., Saitoh,D. and Takeda,K. Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002) Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshinai@genes.nig.ac.jp.
Location/Qualifiers
1..420 /organism="Hordeum vulgare subsp. vulgare" /mol_type="mRNA" /cultivar="Haruna Nijo" /sub_species="vulgare" /db_Xref="itaxon:1125039" /clone="baa19005" /tissue="top three leaves" /dev_stage="adult, heading stage" /clone_lib="K", Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"
IGIN
alignment Scores:
ed. No. : 567 score: 68.00 reference: 100.00% 1st Local Similarity: 100.00% every Match: 74.73% : 9 :
Length: 420 Matches: 8 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0
-09-444-281-35 (1-13) x AV933841 (1-420)
5 TrpProTrpTrpProTrpArgArg 12 186 TGGCCGTGGGCCGTGGCGGA 163
ISOLT 12 471261/c JCUS
DEFINITION BU471261 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves <i>Hordeum vulgare</i> subsp. <i>vulgare</i> cDNA sequence.
BU471261.1 GI:21149764
EST WORDS <i>Hordeum vulgare</i> subsp. <i>vulgare</i> <i>Hordeum vulgare</i> subsp. <i>vulgare</i> Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticeae; <i>Hordeum</i> . 1 (bases 1 to 440)
Sato,K., Saitoh,D. and Takeda,K. Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002) Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855

```

FEATURES          Email: tsnini@genes.nig.ac.jp.
                  Location/Qualifiers
source           1. . 440
                  /organism="Hordeum vulgare subsp. vulgare"
                  /mol_type="mRNA"
                  /cultivar="Haruna Nijo"
                  /sub_species="vulgare"
                  /db_xref="taxon:112509"
                  /clone="baali710"
                  /tissue_type="top three leaves"
                  /dev_stage="adult, heading stage"
                  /clone_lib="K. Sato unpublished CDNA library"
                  /clone="K. Sato unpublished CDNA library"
                  Nijo adult, heading stage top three leaves

ORIGIN

Alignment Scores:
Pred. No.:      599          Length: 440
score:          68.00         Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    74.73%       Indels: 0
DB:             12           Gaps: 0

RESULT 13
AU089922/c     AU089922 446 bp mRNA linear
DEFINITION      AU089922 Hordeum vulgare subsp. vulgare Upper three
                 heading stage Hordeum vulgare subsp. vulgare cDNA c
                 haruna lib1_121 mRNA sequence.
ACCESSION      AU089922.1  GI:7613350
VERSION        EST.
KEYWORDS       Hordeum vulgare subsp. vulgare
SOURCE         Hordeum vulgare subsp. vulgare
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Po
                  Pooidae; Triticeae; Hordeum.
REFERENCE      1 (bases 1 to 446)
AUTHORS        Sato, K., Takahashi, H. and Takeda, K.
TITLE          Hordeum vulgare subsp. vulgare cDNA clone
Unpublished (2000)
COMMENT        Contact: Kazuhiro Sato
                  Research Institute for Bioresources
                  Okayama University, Barley Germplasm Center
                  Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
                  Email: katsato@ribi.okayama-u.ac.jp,
                  URL: http://www.ribi.okayama-u.ac.jp/barley/.
FEATURES        Location/Qualifiers
source           1. . 446
                  /organism="Hordeum vulgare subsp. vulgare"
                  /mol_type="mRNA"
                  /cultivar="Haruna Nijo"
                  /sub_species="vulgare"
                  /db_xref="taxon:112509"
                  /clone="haruna lib1_121"
                  /tissue_type="Upper three leaves at heading
                  /clone_lib="K. Sato unpublished CDNA library"
                  /clone="K. Sato unpublished CDNA library"
                  leaves at heading stage"

ORIGIN

Alignment Scores:
Pred. No.:      608          Length: 446
Score:          68.00         Matches: 8
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    74.73%       Indels: 0
DB:             9            Gaps: 0

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US-09-444-281-35 (1-13) x AU089922 (1-446)

Qy 5 TrpProTrpProTrpArgArg 12
 Db 188 TGGCCTGTTGGCTGGCGCA 165

RESULT 14
 AU198144/c AU198144 446 bp mRNA linear EST 03-APR-2002
 DEFINITION AU198144 Rice green shoot *Oryza sativa* (japonica cultivar-group)
 CDDNA clone S15951, mRNA sequence.

ACCESSION AU198144
 VERSION AU198144.1 GI:14714211
 KEYWORDS EST
 ORGANISM SOURCE *Oryza sativa* (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group); Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; *Oryzaeae*; *Oryza*.

REFERENCE 1 (bases 1 to 446)
 AUTHORS Sasaki, T. and Yamamoto, K.
 TITLE Rice cDNA from green shoot (2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Takuji Sasaki
 National Institute of Agrobiological Resources
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
 305-8602, Japan
 Tel: 81-298-36-7441
 Fax: 81-298-36-7168
 Email: tsasaki@abr.affrc.go.jp, URL: http://rsp.dna.affrc.go.jp/
 PROJECT = 'RGP'

FEATURES source
 PROJECT = 'RGP'

ALIGNMENT Scores:
 Pred. No.: 612 Length: 448
 Score: 68.00 Matches: 7
 Percent Similarity: 90.91% Conservative: 3
 Best Local Similarity: 63.64% Mismatches: 1
 Query Match: 74.73% Indels: 0
 DB: 9 Gaps: 0

US-09-444-281-35 (1-13) x AU198162 (1-448)

Qy 3 LysLysTrpProTrpProTrpArgArgLys 13
 Db 314 CGCCCTGACCTGGCTTGACCGGG 282

SEARCH completed: May 11, 2004, 16:56:32
 Job time : 1725.2 secs

ORIGIN

ALIGNMENT Scores:
 Pred. No.: 608 Length: 446
 Score: 68.00 Matches: 7
 Percent Similarity: 90.91% Conservative: 3
 Best Local Similarity: 63.64% Mismatches: 1
 Query Match: 74.73% Indels: 0
 DB: 9 Gaps: 0

US-09-444-281-35 (1-13) x AU198144 (1-446)

Qy 3 LysLysTrpProTrpProTrpArgArgLys 13
 Db 351 CGCCCTGACCTGGCTTGACCGGG 319

RESULT 15
 AU198162/c AU198162 AU198162 448 bp mRNA linear EST 03-APR-2002
 DEFINITION AU198162 Rice Green shoot *Oryza sativa* (japonica cultivar-group)
 CDDNA clone S16019, mRNA sequence.

ACCESSION AU198162
 VERSION AU198162.1 GI:14714231
 KEYWORDS EST
 SOURCE *Oryza sativa* (japonica cultivar-group)
Oryza sativa (japonica cultivar-group); Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; *Oryzaeae*; *Oryza*.

REFERENCE 1 (bases 1 to 448)
 AUTHORS Sasaki, T. and Yamamoto, K.
 TITLE Rice cDNA from green shoot (2001)

PC	C12N15/09, C07K1/12, C07K1/18, C12N1/15, C12N1/19, C12N1/21, C12P21/02/
PC	(C12P21/02, C12R1:19), C12N15/00
CC	Synthesized oligonucleotide used as a template for PCR FH
Key	Location,Qualifiers
FT source	1..114 /organism='Artificial Sequence' .
FT	Location/Qualifiers
	1..114 /organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
FEATURES	ORIGIN
source	Alignment Scores: Prod. No.: 0..0286 Length: 114 Score: 86.00 Matches: 12 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0
US-09-444-281-36 (1-12) x BD247529 (1-114)	
Qy	1 IleLeuArgTrpProTrpPheProTrpArgArgLys 12
Db	47 ATTCTGCGTTGGCGCTGGTGGCCGCTGGCGTGGCAA 82
RESULT 3	
BD247520	BD247520 151 bp DNA linear PAT 17-JUL-2003
LOCUS	Method for effectively producing antibacterial cationic peptides in host cells.
DEFINITION	
BD247520	BD247520..1 GI:33057290
ACCESSION	
VERSION	JP 2002530114 A/14.
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	artificial sequences.
REFERENCE	1. (bases 1 to 151)
AUTHORS	Burian, J. and Bartfeld, D.
TITLE	Method for effectively producing antibacterial cationic peptides in host cells
JOURNAL	Patent : JP 2002530114-A 14 17-SEP-2002;
COMMENT	MICROLOGIX BIOTECH INC
OS	Artificial Sequence
PN	JP 2002530114-A/14
PD	17-SEP-2002
PP	19-NOV-1999 JP 200054088
PR	20-NOV-1998 US 60/109218
PI	JAN BURIAN, DANIEL BARTFELD
PC	C12N15/09, C07K1/12, C07K1/18, C12N1/15, C12N1/19, C12N1/21, C12P21/02/
PC	(C12P21/02, C12R1:19), C12N15/00
CC	Synthesized oligonucleotide used as a template for PCR FH
Key	Location,Qualifiers
FT source	1..151 /organism='Artificial Sequence' .
FT	Location/Qualifiers
	1..151 /organism="synthetic construct"
	/mol_type="genomic DNA"
	/db_xref="taxon:32630"
FEATURES	ORIGIN
source	Alignment Scores: Prod. No.: 0..0382 Length: 151 Score: 86.00 Matches: 12 Percent Similarity: 100.00% Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0

US-09-444-281-36 (1-12) x BD247520 (1-151)	FEATURES	FEATURES	FEATURES
Qy 1 IleLeuArgTrpProTrpProTrpArgArgLys 12	source	source	source
Db 41 ATTCTCGTGGCCCTGGCTCCAAA 76			
RESULT 4			
BD247517	BD247517	BD247517	BD247517
LOCUS	114 bp	DNA	linear
DEFINITION	Method for effectively producing antibacterial cationic peptides in host cells.	Method for effectively producing antibacterial cationic peptides in host cells.	Method for effectively producing antibacterial cationic peptides in host cells.
ACCESSION	BD247517	BD247517	BD247517
VERSION	GI:33057287	GI:33057287	GI:33057287
SOURCE	JP 2002530114-A1/11	JP 2002530114-A1/11	JP 2002530114-A1/11
ORGANISM	synthetic construct	synthetic construct	synthetic construct
REFERENCE	1 (bases 1 to 114)	1 (bases 1 to 114)	1 (bases 1 to 114)
AUTHORS	Burian,J. and Bartfeld,D.	Burian,J. and Bartfeld,D.	Burian,J. and Bartfeld,D.
TITLE	Method for effectively producing antibacterial cationic peptides in host cells	Method for effectively producing antibacterial cationic peptides in host cells	Method for effectively producing antibacterial cationic peptides in host cells
JOURNAL			
COMMENT			
OS	MICROLOGIX BIOTECH INC	MICROLOGIX BIOTECH INC	MICROLOGIX BIOTECH INC
PN	JP 002530114-A1/11	JP 002530114-A1/11	JP 002530114-A1/11
PD	17-SEP-2002	17-SEP-2002	17-SEP-2002
PF	19-NOV-1999	20-NOV-1998	20-NOV-1998
PR	US 6/109218	US 6/109218	US 6/109218
PI	JAN BURIAN, DANIEL BARTFELD	JAN BURIAN, DANIEL BARTFELD	JAN BURIAN, DANIEL BARTFELD
PC	C12N15/09 C07K1/12, C07K1/18, C12N1/15, C12N1/19, C12N1/21, C12P21/02 //	C12N15/09 C07K1/12, C07K1/18, C12N1/15, C12N1/19, C12N1/21, C12P21/02, C12P21/02, C12P21/19, C12N15/00	C12N15/09 C07K1/12, C07K1/18, C12N1/15, C12N1/19, C12N1/21, C12P21/02, C12P21/02, C12P21/19, C12N15/00
CC	Synthesized oligonucleotide used as a template for PCR FH	Synthesized oligonucleotide used as a template for PCR FH	Synthesized oligonucleotide used as a template for PCR FH
Key	Location/Qualifiers	Location/Qualifiers	Location/Qualifiers
FT	1..114	1..114	1..114
source	/organism='Artificial Sequence'	/organism='Artificial Sequence'	/organism='Artificial Sequence'
FT			
FEATURES			
source			
ORIGIN			
Alignment Scores:			
Pred. No.:	0.532	Length:	114
Score:	75.00	Matches:	9
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	90.00%	Mismatches:	0
Query Match:	87.21%	Indels:	0
DB:	6	Gaps:	0
US-09-444-281-36 (1-12) x BD247517 (1-114)			
Qy 3 ArgTrpProTrpTrpProTrpArgArgLys 12			
Db 50 AAAAGCCGTTGGCTGGCGCTGGCTGCTAA 79			
RESULT 5			
AX357080	AX357080	AX357080	AX357080
LOCUS	68 bp	DNA	linear
DEFINITION	Sequence 6 from Patent WO2006517.	Sequence 6 from Patent WO2006517.	Sequence 6 from Patent WO2006517.
VERSION	GR:18674262	GR:18674262	GR:18674262
KEYWORD S	synthetic construct	synthetic construct	synthetic construct
ORGANISM	synthetic construct	synthetic construct	synthetic construct
REFERENCE	1 Bylina,E.J., Coleman,W.J. and Youwan,D.C.	1 Bylina,E.J., Coleman,W.J. and Youwan,D.C.	1 Bylina,E.J., Coleman,W.J. and Youwan,D.C.
AUTHORS	High-throughput methods for generating and screening compounds that affect cell viability	High-throughput methods for generating and screening compounds that affect cell viability	High-throughput methods for generating and screening compounds that affect cell viability
TITLE	Patent: WO 0206517-A 6 24-JAN-2002;	Patent: WO 0206517-A 6 24-JAN-2002;	Patent: WO 0206517-A 6 24-JAN-2002;
JOURNAL	Kairos Scientific, Inc. (US)	Kairos Scientific, Inc. (US)	Kairos Scientific, Inc. (US)
FEATURES			
source			
ORIGIN			
Alignment Scores:			
Pred. No.:	0.665	Length:	39
Score:	70.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	81.40%	Indels:	0
DB:	6	Gaps:	0
US-09-444-281-36 (1-12) x BD128612 (1-39)			
Qy 3 ArgTrpProTrpTrpProTrpArgArgLys 11			
Db 13 AAATGCCCTGGGCCGCGTCGT 39			

RESULT 7
AR404925
LOCUS Sequence 1 from patent US 6630197. DNA
DEFINITION Sequence 1 from patent US 6630197.
ACCESSION AR404925
VERSION AR404925.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1. (bases 1 to 69)
AUTHORS Wood, T.K., Jayaraman, A. and Barthman, J.C.
TITLE Inhibition of sulfate-reducing-bacteria-mediated degradation using
bacteria which secrete antimicrobials
PATENT: US 6630197-A 1 07-OCT-2003;
JOURNAL
FEATURES Location/Qualifiers
Source 1. .69
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.2
Score: 70.00
Percent Similarity: 100.00%
Best Local Similarity: 88.89%
Query Match: 81.40%
DB: 6
US-09-444-281-36 (1-12) x AR404925 (1-69)
Qy 3 ArgTrpProTrpProTrpProTrpArgArg 11
Db 28 AAATGGCTTGGTGGCTGGCTGGCGCGC 54

RESULT 8
AR226388
LOCUS AR226388
DEFINITION Sequence 11 from patent US 6444645. DNA
ACCESSION AR226388
VERSION AR226388.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1. (bases 1 to 211)
AUTHORS Seilsted, M.B. and Osapay, K.
TITLE Crosslink-stabilized indolicidin analogs
PATENT: US 6444645-A 11-03-2002;
JOURNAL
FEATURES Location/Qualifiers
Source 1. .211
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3.79
Score: 70.00
Percent Similarity: 100.00%
Best Local Similarity: 88.89%
Query Match: 81.40%
DB: 6
US-09-444-281-36 (1-12) x AR226388 (1-211)
Qy 3 ArgTrpProTrpProTrpProTrpArgArg 11
Db 38 AAATGGCCGGTGGTGGCGCTGGCGCTGG 64

RESULT 9
AR282754
LOCUS AR282754
DEFINITION Sequence 38 from patent US 6524585.

ACCESSION AR282754
VERSION AR282754.1
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1. (bases 1 to 211)
AUTHORS Seilsted, M.E.
TITLE Indolicidin analogs and methods of using same
PATENT: US 6524585-A 28-25-FEB-2003;
JOURNAL
FEATURES Location/Qualifiers
Source 1. .211
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 3.79
Score: 70.00
Percent Similarity: 100.00%
Best Local Similarity: 88.89%
Query Match: 81.40%
DB: 6
US-09-444-281-36 (1-12) x AR282754 (1-211)
Qy 3 ArgTrpProTrpProTrpProTrpArgArg 11
Db 38 AAATGGCGTGGTGGCGCTGGCGCTGG 64

RESULT 10
BTINDLCD
LOCUS BTINDLCD
DEFINITION Bos taurus mRNA for cathelicidin (CATHL4 gene).
ACCESSION X67340
VERSION X67340.1
KEYWORDS cathelicidin; CATHL4 gene; indolicidin antimicrobial peptide.
SOURCE Bos taurus (cow)
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Etheria; Chordiota; Actydia; Ruminantia; Peccora; Bovoidea; Bovidae; Bovinae; Bos.
REFERENCE
AUTHORS Del Sal, G., Storici, P., Schneider, C., Romeo, D., and Zanetti, M.
TITLE cDNA cloning of the neutrophil bactericidal peptide indolicidin
JOURNAL Biochem. Biophys. Res. Commun. 187 (1), 467-472 (1992)
MEDLINE 92392368
PUBMED 1520337
REFERENCE
AUTHORS Del Sal, G.
TITLE Direct Submission (20-JUL-1992) G. Del Sal, Univ. of Trieste, Dip. di Biochimica, Biotecnica e Chimica delle Macromolecole, Via A. Valerio, 38, 34127 Trieste, Italy
JOURNAL
FEATURES Location/Qualifiers
Source 1. .550
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/cell_line="bone marrow cells"
1. .550
/gene="CATHL4"
13 .447
/gene="CATHL4"
/function="indolicidin antimicrobial peptide"
/codon_start=1
/product="cathelicidin"
/protein_id="CRA47755.1"
/db_xref="GI:463"
/db_xref="GO:033046"
/db_xref="SWISS-PROT:P33046"
/translation="MOTQASLISLGWSWMLLGLYVPSASAQLSSTRAVLRAVDQ
IENLSESEANLRLLELDPPKNDIGTRKPVSTVKEVPTIQPAEQCDFKKG

JOURNAL	Patent: WO 0119969-A 5 22-MAR-2001;				
FEATURES	Large Scale Biology Corporation (US)				
FEATURES	Location/Qualifiers				
Source	1. .6446 /organism="Nicotiana benthamiana" /mol_type="unassigned RNA" /db_xref="taxon:4100"				
ORIGIN					
Alignment Scores:					
Pred. No.:	129	Length:	6446		
Score:	70.00	Matches:	8		
Percent Similarity:	100.00%	Conservative:	1		
Best Local Similarity:	88.89%	Mismatches:	0		
Query Match:	81.40%	Indels:	0		
DB:	6	Gaps:	0		
US-09-444-281-36 (1-12) x AX098418 (1-6446)					
Qy	3 ArgGtpProtPTrpProtPArgGarg 11				
Db	6213 AAGGGCTCTGGCCATGGCGCGA 6239				
RESULT 13					
AL672300	AL672300	149981 bp	DNA	linear	ROD 14-JUN-2000
LOCUS	DEFINITION	Mouse DNA sequence from clone RP23-446K8 on chromosome X, complete sequence.			
AL672300	AL672300	149981			
VERSION	VERSION	GI:21436714			
KEYWORDS	KEYWORDS	Mus musculus (house mouse)			
ORGANISM	ORGANISM	Mus musculus			
REFERENCE	REFERENCE	1. (bases 1 to 149981)			
AUTHORS	AUTHORS	Tracey,A.			
TITLE	TITLE	Direct Submission			
JOURNAL	JOURNAL	Submitted (14-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SE, UK. E-mail enquiries: clonerrequest@sanger.ac.uk			
COMMENT	COMMENT	humgpry@sanger.ac.uk Clone requests: clonerrequest@sanger.ac.uk			
		On Jun 17, 2002 this sequence version replaced gi:2261839.			
		During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.			
		This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Mp: WORMPP; Information on the WORMPP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpp RP23-446K8 is from the RPCI-23 Mouse PAC Library			
FEATURES	FEATURES	For further details see http://www.chori.org/bacpac/home.htm			
VECTOR	VECTOR	VECTOR: pBAC8.6.			
FEATURES	FEATURES	Location/Qualifiers			
Source	1. 149981 /organism="Mus musculus" /mol_type="Genomic DNA" /db_xref="taxon:10090" /chromosome="X" /clone="RP23-446K8" /clone_id="RPCI-23"				
ORIGIN					

site: sequence:BZ164864¹
 end sequence:105081..110233
 /note=wgs_contig"

misc_feature

ORIGIN

Alignment Scores:

Pred. No.:	4.34e+03	Length:	195764
Score:	70.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	81.40%	Indels:	0
DB:	2	Gaps:	0

US-09-444-281-36 (1-12) x AC113900 (1-195764)

Qy 3 ArgGtpProGtpProGtpArgArg 11

Db 187911 AGTGGCCATGGGCCATGGAGCGCG 187937

RESULT 15

AC095460 LOCUS Rattus norvegicus clone CH230-7JB, WORKING DRAFT SEQUENCE.

DEFINITION Rattus norvegicus clone CH230-7JB, WORKING DRAFT SEQUENCE.

AC095460 AC095460 GI:30467723

AC095460 AC095460 HTGS_DRAFT; HTGS_FULLTOP.

VERSION HTGS: HTGS_PASEF; HTGS rat

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 255121)

REFERENCE

AUTHORS Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Alien, C., Allen, H., Alshabani, A., Amin, A., Arquiano, D., Anyabebche, V., Ailen, H., Akyoglu, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, F., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavarozzi, I., Ceasar, H., Center, A., Chacko, J., Chavee, D., Chen, G., Chen, R., Chen, Z., Chiu, J., Cleveland, C., Cookrell, R., Cox, C., Coville, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy Carroll, L., De Ando, C., Dederich, D., Delgado, O., Denison, S., Derano, C., Ding, Y., Dirth, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Dyal, B., Eaves, K., Egan, A., Escott, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandes, S., Finley, M., Flagg, N., Fortes, J., Fosser, M., Fosser, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebrgeorgis, E., Gear, K., Gill, J.R., Grady, M., Guerra, W., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havia, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulky, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Jolivet, A., Jackson, L., Johnson, R., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, S., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Loresuherwa, L., Louisgehd, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindarne, M., Mahmoud, M., Mallory, K., Margum, A., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, G., Norris, K., Norris, S., Nair, L., Nankervis, C., Neel, D., Newton, N., Nguyen, N., Norris, S., Nwakellemen, O., Okwonu, G., Olarunpasaoglu, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L., Reigh, R., Reilly, M., Quiroz, J., Rachlin, E., Reeves, K., Richards, S., Riggs, P., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scheer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shavarbeyn, A., Sibson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J.,

FEATURES

source

REFERENCE

Authors

Authors

COMMENT

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequence reads assembled using Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.edu/>
 Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GCJK

Center clone name: CH230-7JB

Summary Statistics

Assembly program: Atlas;
 Assembly size: 243844 bases at least 040
 Consensus quality: 245664 bases at least Q30
 Consensus quality: 246956 bases at least Q20
 Estimated insert size: 7x in Q20 bases; sum-of-contigs estimation
 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
 * NOTE: This sequence may represent more than one clone.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1. 255121: contig of 255121 bp in length.
 * Location/Qualifiers
 * 1. .255121
 * /note="genomic DNA"
 * /note="Rattus norvegicus"
 * /note="wgs contig"
 * /note="wgs contig"
 * /note="wgs contig"

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11; indolicidin; bovine; ss.

RESULT 1
AAA27296 standard; DNA; 108 BP.
ID AAA27296
IV

RESULT 1
AAA27296
ID AAA
XX

WPPI; 2000-40086/34.
Multi-domain fusion protein expression cassette used for high yield
stable production of foreign peptide gene products.

PS Example 5; Page 39; 73pp; English.
 XX A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin

SQ Sequence 108 BP; 18 A; 33 C; 31 G; 26 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.0254 Length: 108
 Score: 86.00 Matches: 12
 Percent. Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-444-281-36 (1-12) x AAA27298 (1-108)

Qy 1 IleLeuArgTrpProTrpProTrpProTrpArgLys 12
 DB 41 ATTCCTGGTGGCCCTG3TGGCGTGGCGCTCGAAA 76

RESULT 2
 ID AAA27298 standard; DNA; 114 BP.
 XX

AC AAA27298;

XX DT 20-SEP-2000 (first entry)

XX DE Oligonucleotide used for synthesis of MBI 11B7 first cassette.
 XX KW Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11;
 KW indolicidin; bovine; ss.
 XX CS Synthetic.
 XX PN WO200031279-A2.
 XX PD 02-JUN-2000.

XX PF 19-NOV-1999; 99WO-CA001107.

XX PR 20-NOV-1998; 98US-0109218P.

XX DR 2000-400086/34.

XX PT Multi-domain fusion protein expression cassette used for high yield

XX PT stable production of foreign peptide gene products.

XX PS Example 5; Page 38; 73pp; English.

XX PA (MICR-) MICROLOGIX BIOTECH INC.

XX PI Burian J, Bartfeld D;

XX DR 2000-400086/34.

XX PT Multi-domain fusion protein expression cassette used for high yield
 XX PS Example 5; Page 40; 73pp; English.
 XX A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic peptides such as bovine indolicidin may

CC be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin

SQ Sequence 114 BP; 20 A; 34 C; 32 G; 28 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.0269 Length: 114
 Score: 86.00 Matches: 12
 Percent. Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-444-281-36 (1-12) x AAA27298 (1-114)

Qy 1 IleLeuArgTrpProTrpProTrpProTrpArgArgLys 12
 DB 47 ATTCCTGGTGGCCCTG3TGGCGTGGCGCTCGAAA 82

RESULT 3
 ID AAA27294

XX ID AAA27294 standard; DNA; 151 BP.

XX AC AAA27294;

XX XX 20-SEP-2000 (first entry)

XX DS Oligonucleotide used for synthesis of MBI 2X11B7 last cassette.

XX XX Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11;

XX KW indolicidin; bovine; ss.

XX OS Synthetic.

XX PN WO200031279-A2.

XX XX 02-JUN-2000.

XX PD 19-NOV-1999; 99WO-CA001107.

XX XX 20-NOV-1998; 98US-0109218P.

XX XX (MICR-) MICROLOGIX BIOTECH INC.

XX PI Burian J, Bartfeld D;

XX DR WPI; 2000-400086/34.

XX PT Multi-domain fusion protein expression cassette used for high yield

XX PT stable production of foreign peptide gene products.

XX PS Example 5; Page 38; 73pp; English.

XX PA (MICR-) MICROLOGIX BIOTECH INC.

A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin

SQ Sequence 151 BP; 22 A; 44 C; 49 G; 36 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0.0361 Length: 151
 Score: 86.00 Matches: 12

Percent Similarity:	100.00%	Conservative:	0	QY	3 ArgTyrProIleProIleProIleArgArgLys	12
Best Local Similarity:	100.00%	Mismatches:	0	DB	:::	
Query Match:	100.00%	Indels:	0		34 AAATGGCGTGTGCGCTGCGTCCTAAA	63
DB:	3	Gaps:	0			
US-09-444-281-36 (1-12) x AAA27294 (1-151)				RESULT 5		
QY	1 IleLeuArgTyrProIleProIleProIleArgArgLys	12		ID	AAA27291 standard; DNA; 114 BP.	
DB	41 ATTCGCGTGGCGTGGCGCTGCGTCCTAAA	76		AC	AAA27291;	
RESULT 4				XX		
ID	AAV60908 standard; DNA; 88 BP.			XX	Oligonucleotide used for synthesis of MBI-11 fragment.	
XX	AAV60908;			XX	Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11;	
AC				XX	indolicidin; bovine; ss.	
XX				OS		
DT	11-JAN-1999 (first entry)			XX	Synthetic.	
XX				PN	WO2000031279-A2.	
DB	DNA fragment encoding MBI11.			XX		
XX				PD	02-JUN-2000.	
KW	MBI28; cationic peptide; Plasmid pXCL1; small cryptic plasmid;			XX		
KW	replication; RepA; vector; RAMP; human; MBI11; ss.			PF	19-NOV-1999; 99WO-CA001107.	
XX				XX		
OS	Synthetic.			PR	20-NOV-1998; 98US-0109218P.	
OS	Homo sapiens.			XX		
XX				PA	(MICR-) MICROLOGIX BIOTECH INC.	
PN	WO9841636-A2.			XX		
XX				PD	Burian J., Bartfeld D;	
PD				XX		
XX				PI	Burian J., Bartfeld D;	
24-SEP-1998.				XX		
XX				DR	WPI; 2000-400086/34.	
PP	16-MAR-1998; 98WO-CA000214.			XX	Multi-domain fusion protein expression cassette used for high yield	
PP				PT	stable production of foreign peptide gene products.	
PR	14-MAR-1997; 97US-0040722P.			XX		
XX				PS	Example 4; Page 37; 73pp; English.	
PA	(BURJ/)			XX		
PA	(KAYW/)			CC	A novel method allows the efficient production of cationic peptides in	
PA	KAY W. W.			CC	recombinant host cells. The method involves construction of a multi-	
XX				CC	domain fusion protein expression cassette comprising a promoter and a	
DR	WPI; 1998-53151/45.			CC	nucleic acid molecule expressed as an insoluble protein. The inclusion of	
XX				CC	anionic peptide sequences in the linker sequences neutralises the	
PR	Increasing plasmid copy number in a cell with the repA gene product - and			CC	positive charge of the cationic peptide so that the charge of the fusion	
PR	pr			CC	protein is controlled. This cassette allows high yield, stable production	
PR	pr			CC	of the cationic peptide. Cationic peptides such as bovine indolicidin may	
PR	pr			CC	be used as antimicrobial agents. The present sequence is an	
PR	pr			CC	oligonucleotide that was used to synthesise a MBI-11 fragment. MBI-11 is	
PS	Example 16; Page 57; 82pp; English.			CC	a cationic peptide derived from modifications of indolicidin	
XX				XX	Sequence 114 BP; 25 A; 26 C; 30 G; 33 T; 0 U; 0 Other;	
CC	This oligonucleotide was used as a template in a PCR reaction (see also			Alignment Scores:		
CC	CC AAV60909-10) to generate a DNA fragment encoding the cationic peptide			Pred. No.:	0.523	Length: 114
CC	CC MBI11 (see AAW71690). The PCR product was cloned into the universal			Score:	75.00	Matches: 9
CC	CC vector pR21-B1, which contains the R21 replication leader of RepA (see			Percent Similarity:	100.00%	Conservative: 1
CC	CC AAW71686) and 2 tandem copies of the prepro region (Hpro) of human			Best Local Similarity:	90.00%	Mismatches: 0
CC	CC defensin. The vector provides expression of R21-hpro-MBI11 fusion in host			Query Match:	87.21%	Indels: 0
CC	CC cells. The invention provides controlled replication plasmid vectors			DB:	3	Gaps: 0
CC	CC (RAMP vectors) comprising a replication origin of a small cryptic plasmid					
CC	CC such as pXCL1 (see AAW71686). The					
CC	CC vectors can reach very high levels of plasmid replication, but are not					
CC	CC lethal to the host cell, and can be used to direct the high level					
CC	CC expression of e.g. cytokines, antigens and therapeutic proteins					
XX	Sequence 88 BP; 20 A; 18 C; 25 G; 25 T; 0 U; 0 Other;					
SQ						
Alignment Scores:						
Pred. No.:	0.399	Length:	88			
Score:	75.00	Matches:	9			
Percent Similarity:	100.00%	Conservative:	1			
Best Local Similarity:	90.00%	Mismatches:	0			
Query Match:	87.21%	Indels:	0			
DB:	2	Gaps:	0			
US-09-444-281-36 (1-12) x AAV60908 (1-88)						
QY	3 ArgTyrProIleProIleProIleArgArgLys	12				
DB	:::					
50 AAATGGCGTGTGCGCTGCGTCCTAAA	79					
RESULT 6						
ID	AAI72481 standard; cDNA; 68 BP.					
AC						
XX						
DT	16-MAY-2002 (first entry)					

DE DNA fragment of the invention #15.
XX Gene expression; peptide antibiotic; purF gene; ds.
KW

PF 08-JUN-2001; 2001KR-000031889.
XX
PR 08-JUN-2001; 2001KR-000031889.
YY

2008-JUN-2001; 2001KR-00031889.
XX (SAMYANG) SAMYANG GENEX CORP.
XX Hong SS, Kang MH, Kim JH, Lee HS, Lee JW, Park SH;
XX PPI PI XX WPI; 2002-301977/34.
XX XX Gene expression system useful for mass-production of peptide antibiotics
XX and vectors derived from microorganisms.

XX Disclosure; Page 7; 56PP; Korean.

The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The generic component consists of a first gene sequence which codes for the whole or partial peptide antibiotic, and a second gene sequence which codes for a peptide gene or its derivative, and a second gene sequence which codes for a peptide antibiotic. The mass-production method of peptide antibiotics comprises the steps of: constructing an expression vector including the genetic component, transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of PGNY2, PGNY4 and PGNY5, and it has a high copy number of origin, strong transcription promoter and structural genes. The sequences given in records ABL60400-ABL60464 represent DNA sequences of the invention.

XX SO Semience 47 BP: 6 A: 11 C: 19 G: 11 T: 0 U: 0 Other: 0

Alignment Scores:	
Pred. No.:	0.795
Score:	70.00
Percent Similarity:	100.00%
Best Local Similarity:	88.19%
Query Match:	81.40%
DB:	6

XX Unidentified.
XX KR2001098973-A.
XX 08-NOV-2001.
XX

Digitized by srujanika@gmail.com

XX 09-JUN-1998; 98KR-000222117.
 XX PR 14-MAY-1998; 99KR-00011920.
 XX (SAMYANG) SAMYANG GRNEX CORP.
 XX
 XX P1 Kim JH, Kang MH, Lee J, Park SH, Lee JW, Hong SS, Lee H;
 XX WPI, 2000-097542/08.
 XX P-PSDB; AAY44324.
 XX
 XX New DNA constructs useful for mass production of antimicrobial peptides
 XX in microorganism hosts.
 XX
 XX P1 Fig 1; 67pp; English.
 XX
 XX The present DNA sequence encodes an antimicrobial peptide, Indolicidin
 XX derived from cow, Bos taurus. It is used along with a derivative of purF
 XX gene sequence that functions as a fusion partner. A DNA construct that
 XX comprises this antimicrobial peptide encoding sequence and the entire,
 XX partial or derivative of purF gene, is used for mass production of the
 XX antimicrobial peptide in microorganisms without killing the host cells.
 XX Use of the purF gene derivative sequence, neutralises the toxicity of the
 XX antimicrobial peptides against the host microorganisms. The antimicrobial
 XX peptides are useful commercially in the pharmaceutical and food
 XX industries

ence 53. BP; 8 A; 12 C; 20 G; 13 T; 0 U; 0 Other;

Alignment Scores:	0.902	Length:	53
Preferred No.:	70.00	Matches:	8
Score:	100.00%	Conservative:	1
Overall Similarity:	88.89%	Mismatches:	0
Nearest Local Similarity:	88.89%	Indels:	0
Boundary Match:	81.40%	Gaps:	0
BB:	3		

US-09-444-281-36 (1-12) x AAZ29364 (1-53)

RESULT 13
ABL60445 standard; DNA; 53 BP.
ABL60445
XX
XX
AC
XX
XX
ABL60445;
28-MAR-2003 (first entry)
DNA fragment of the invention #44.
Gene expression; peptide antibiotic; purF gene; ds.

```
Location/Qualifiers  
5 .60 /*tag= a  
partial
```

XX KKR2001099973-A.
XX SDN 08-NOV-2001.
XX PDP 08-JUN-2001; 2001KR-00031889.
XX PPP 08-JUN-2001; 2001KR-00031889.
XX PR 08-JUN-2001; 2001KR-00031889.
XX (SAMY-) SAMYANG GENEX CORP.
XX

P11 Hong SS, Kang MH, Kim JH, Lee HS, Lee JW, Park SH;
 XX WPI: 2002-101977/34.
 DR P-PSDB; ABB81940.
 XX
 P12 Kim JH, Park SH;
 XX Disclosure; Page 17; 56pp; Korean.
 XX
 The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial peptide antibiotic, and a second gene sequence which codes peptide antibiotics. The mass-production method of peptide antibiotics comprises the steps of: constructing an expression vector including the genetic component, transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of PGKX2, PGKX4 and PGKX5, and it has a high copy number of origin, strong transcription promoter and structural genes. The sequences given in records AB040400-ABL60464 represent DNA sequences of the invention
 XX
 Sequence 53 BP; 8 A; 12 C; 20 G; 13 T; 0 U; 0 Other;
 XX

Alignment scores:		Length:	
Pred. No.:	0.902	Matches:	53
Score:	70.00	Conservative:	8
Percent. Similarity:	100.00%	Mismatches:	1
Best Local Similarity:	88.9%	Indels:	0
Query Match:	81.40%	Gaps:	0
DB:	6		
US-09-444-281-36 (1-12) x ABL60445 (1-53)			
Qy	3 ArgTrpProIrpTrpProTrpArgArg	11	
	::: : : : : : : :		
Db	17 AATGGCGGTTGGCCGTGGGTGT	43	

RESULT 14
 AAZ40246 standard; DNA; 69 BP.
 ID AAZ40246
 XX
 AC AAZ40246;
 XX
 XX 23-FEB-2000 (First entry)
 DT
 XX Oligonucleotide for cloning indolicidin peptide coding sequence.
 DE
 XX Indolicidin; bactericin; sulphate-reducing bacteria; growth inhibitor;
 KW corrosion; degradation; metal; concrete; dental implant; biofilm;
 SS.
 KW
 XX

US
Bacillus sp.
XX
WO9956553-A1.
XX
11-NOV-1999.
XX
03-MAY-1999;
XX
06-MAY-1998;
PR
31-MAR-1999;
XX
(REGC) UNITY CALIFORNIA.
PA
Wood TK, Jayaraman A, Earthman JC;
XX
WPI; 2000-052882/04.
XX
PR
XX
Inhibiting growth of sulfate-reducing bacteria using other bacteria.

PT Particularly for protection of metals and concrete.
 PS Example 4; Fig 1; 84pp; English.
 XX This sequence represents an oligonucleotide for cloning the non-amidated indolicidin peptide coding sequence. The invention relates to a method for inhibiting growth of sulphate-reducing bacteria (A) on a material (B) sensitive to corrosion or degradation, by applying to (B) a bacterium (C) that secretes a compound (I) able to inhibit growth of (A). The method is used to protect metal, concrete or cement against corrosion and degradation, but (B) can also be used to protect dental implants, (B) is present in an open or closed system (e.g. water cooling tower, liquid storage container, fuel tank, sewer or drainage system etc.) or part of a bridge or other structure. The method is more effective and less expensive than known methods for inhibiting (A), and reduces the amount of toxic chemicals released. Conventional biofilms of aerobic organisms tend to encourage growth of (A), and addition of (C) to the biofilm prevents this. A single application of (C) lasts for a long time, and (I) are produced exactly where they are required and inhibit (A) without significant impact on other organisms (this effect includes reducing resistance of (A) to conventional biocides, which may then be used in reduced amounts). If local damage to the biofilm occurs, the underlying material is still protected by diffusion of (I) from neighbouring areas
 XX Sequence 69 BP; 14 A; 18 C; 20 G; 17 T; 0 U; 0 Other;
 SQ

Alignment Scores:

Pred. No.: 1.19 Length: 69
 Score: 70.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 88.88% Mismatches: 0
 Query Match: 81.49% Indels: 0
 DB: 3 Gaps: 0

US-09-444-281-36 (1-12) x AA440246 (1-69)

QY 3 ArgTrpProItpTrpProTrpArgArg 11
 :::|||||:|||||:|||||:|||||:|||||:|||||:
 Db 28 AAATGGCTTGTGGCCTTGCC 54

RESULT

ARZ49764

ID AAZ49764 standard; DNA; 211 BP.

XX

AC AAZ49764;

XX

DT 18-APR-2000 (First entry)

XX

DE Poly-(Indol (1-13)-Met-Ala-Arg-Ile-Ala-Met)3 DNA.

XX

KW Crosslinked indolicidin analog; X-indolicidin; poly-Indol 1-13; stability; bovine neutrophil; antimicrobial; fungicide; protozoacide; virucide; anti-HIV; human immunodeficiency virus-1; HIV-1; KW positive bacteria; gram negative; Staphylococcus aureus; Escherichia coli; Salmonella typhimurium; yeast; fungi; Protozoa; Candida albicans; Cryptococcus neoformans; Giardia; Acanthamoeba; hexapeptide spacer; ds.

XX

OS Synthetic.

OS Bcs sp.

XX

FH Key

primer_bind

CDS

/tag= b

/tag= a

/product= "Poly-(Indol(1-13)-Met-Ala-Arg-Ile-Ala-Met)3"

/note= "encodes three copies of Indol 1-13, each separated by Met-Ala-Arg-Ile-Ala-Met spacer sequence"

68 .71

/tag= d

/note= "corresponds to overlap in oligonucleotides used for ligation"

FT misc_feature 148 .151
 FT /*tag= e
 FT /note= "corresponds to overlap in oligonucleotides used
 CC for ligation"
 CC complement (191. .211)
 CC /*tag= c
 XX W09965510-A1.
 XX PD 23-DEC-1999.
 XX PP 20-MAY-1999;
 XX DR 9900-US011165.
 XX PR 18-JUN-1998;
 XX DR 98US-00095631.
 XX PA (REBC) UNIV CALIFORNIA.
 XX PI Seisted ME, Osapay K;
 XX DR WPI; 2000-147133/13.
 XX DR P-PSDB; AAX44668.
 XX PA Crosslinked indolicidin analogs with antimicrobial activity against
 PT bacteria, yeast, fungi, protozoa and viruses.
 XX PR Example 1C; Fig 1; 53pp; English.
 XX PS Example 1C; Fig 1; 53pp; English.
 XX CC The patent discloses crosslinked analogs of indolicidin (Indol 1-13) which is a naturally occurring Peptide isolated from bovine neutrophils and has antimicrobial activity. The crosslinked indolicidin (X-indolicidin) analogs are stable and have antimicrobial activity against gram positive and negative bacteria (e.g. Staphylococcus aureus, Escherichia coli and Salmonella typhimurium), yeasts and fungi (e.g. Candida albicans, Cryptococcus neoformans), protozoa (e.g. Giardia species and Acanthamoeba species), and viruses (e.g. HIV-1). They can be used for reducing or inhibiting the growth or survival of microorganisms in an environment e.g. a food or food product, a solution, an inanimate object comprising a surface or a mammal. The present sequence is a DNA encoding a protein comprising three copies of Indol 1-13 each separated by a hexapeptide spacer sequence. The sequence was used to produce a recombinant construct for the expression of Indol-homoserine (Hse) analog. The ability of Indol-Hse analog to maintain antimicrobial activity provides a means to produce X-indolicidin analog precursors in sufficient quantities
 XX SQ Sequence 211 BP; 36 A; 50 C; 74 G; 51 T; 0 U; 0 Other;
 XX Alignment Scores:
 CC Fred. No.: 3.84 Length: 211
 CC Score: 70.00 Matches: 8
 CC Percent Similarity: 100.00% Conservative: 1
 CC Best Local Similarity: 88.89% Mismatches: 0
 CC Query Match: 81.40% Indels: 0
 CC DB: 3 Gaps: 0
 XX US-09-444-281-36 (1-12) x AAZ49764 (1-211)
 CC Qy 3 ArgTrpProItpTrpProTrpArgArg 11
 CC :::|||||:|||||:|||||:|||||:|||||:
 CC Db 38 AAATGGCTTGTGGCCTTGCC 64
 CC Search completed: May 11, 2004, 14:43:52
 CC Job time : 238.12 sec
 CC

13	59	68.6	382	4	US-09-118-554-59	Sequence 59, App1
14	59	68.6	382	4	US-09-118-627-59	Sequence 59, App1
15	59	68.6	382	4	US-09-602-877A-59	Sequence 59, App1
16	59	68.6	383	3	US-09-020-956-82	Sequence 82, App1
17	59	68.6	383	3	US-09-607-82	Sequence 82, App1
18	59	68.6	383	4	US-09-439-313-82	Sequence 82, App1
19	59	68.6	383	4	US-09-352-618A-82	Sequence 82, App1
20	59	68.6	383	4	US-09-232-149A-82	Sequence 82, App1
21	59	68.6	383	4	US-09-159-812-82	Sequence 82, App1
22	59	68.6	383	4	US-09-636-215-82	Sequence 82, App1
23	59	68.6	383	4	US-09-685-166A-82	Sequence 82, App1
24	59	68.6	383	4	US-09-685-166A-82	Sequence 82, App1
25	59	68.6	383	4	US-09-688-489-82	Sequence 82, App1
26	59	68.6	384	4	US-09-030-607-183	Sequence 183, App1
27	59	68.6	384	4	US-09-439-313-183	Sequence 183, App1
28	59	68.6	384	4	US-09-352-616A-183	Sequence 183, App1
29	59	68.6	384	4	US-09-232-149A-183	Sequence 183, App1
30	59	68.6	384	4	US-09-159-812-183	Sequence 183, App1
31	59	68.6	384	4	US-09-215-183	Sequence 183, App1
32	59	68.6	384	4	US-09-685-166A-183	Sequence 183, App1
33	59	68.6	384	4	US-09-115-453-183	Sequence 183, App1
34	59	68.6	384	4	US-09-688-489-183	Sequence 183, App1
35	59	68.6	440	4	US-09-118-554-45	Sequence 45, App1
36	59	68.6	440	4	US-09-118-627-45	Sequence 45, App1
37	59	68.6	440	4	US-09-602-877A-45	Sequence 45, App1
38	59	68.6	499	3	US-09-020-956-73	Sequence 73, App1
39	59	68.6	499	3	US-09-030-607-73	Sequence 73, App1
40	59	68.6	499	4	US-09-439-313-73	Sequence 73, App1
41	59	68.6	499	4	US-09-352-616A-73	Sequence 73, App1
42	59	68.6	499	4	US-09-232-149A-73	Sequence 73, App1
43	59	68.6	499	4	US-09-159-812-73	Sequence 73, App1
44	59	68.6	499	4	US-09-636-215-73	Sequence 73, App1
45	59	68.6	499	4	US-09-685-166A-73	Sequence 73, App1

LENGTH: 88 base pairs
 TYPE: nucleic acid
 STRANDEADS: Single
 TOPOLOGY: linear
 US-09-042-071-49

Alignment Scores:
 Pred. No.: 0.129 Length: 88
 Score: 75.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 9
 Best Local Similarity: 90.00% Mismatches: 0
 Query Match: 87.21% Indels: 0
 DB: 3 Gaps: 0

US-09-444-281-36 (1-12) x US-09-042-071-49 (1-88)

Qy 3 ArgTrpProTrpTrpProTrpArgArgLys 12
 Db 34 AATGGCCGTCGTCCTGGCTGTAA 63

RESULT 2
 US-09-230-180-29

Sequence 29, Application US/09230180

Patent No. 6183992

GENERAL INFORMATION:
 APPLICANT: Kim, Sun-Chang
 Lee, Jae Hyun
 Kang, Min Hyung
 Kim, Jeong Hyun
 Hong, Seung-Suh
 Lee, Hyun-Soo
 APPLICANT: Samyang Genex Corporation
 Korea Advanced Institute of Science and Technology

TITLE OF INVENTION: METHOD FOR MASS PRODUCTION OF
 ANTIMICROBIAL PEPTIDE

FILE REFERENCE: 6181/0F135

CURRENT APPLICATION NUMBER: US/09/230,180

CURRENT FILING DATE: 1999-03-10

PRIOR APPLICATION NUMBER: PCT/KR98/00132

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: KR 13372/1998

PRIOR FILING DATE: 1998-04-09

PRIOR APPLICATION NUMBER: KR 21312/1997

PRIOR FILING DATE: 1997-05-28

NUMBER OF SEQ ID NOS: 36

SEQ ID NO: 29 LENGTH: 39

TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: DNA sequence deduced from Indolicidin Peptide
 US-09-230-180-29

Alignment Scores:
 Pred. No.: 0.209 Length: 39
 Score: 70.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 81.40% Indels: 0
 DB: 3 Gaps: 0

US-09-444-281-36 (1-12) x US-09-230-180-29 (1-39)

Qy 3 ArgTrpProTrpTrpProTrpArgArg 11
 Db 13 AATGGCCGTCGTCCTGGCTGTAA 39

RESULT 3
 US-09-282-277-1
 Sequence 1, Application US/09282277

Patent No. 6630197

GENERAL INFORMATION:
 APPLICANT: Wood, Thomas K.
 APPLICANT: Jayaraman, Arul
 APPLICANT: Barthman, James C.
 APPLICANT: The Regents of the University of California
 TITLE OF INVENTION: Inhibition of Sulfate-Reducing-Bacteria-Mediated Degradation Using Bacteria Which Secrete Antimicrobials

FILE REFERENCE: 023078-095910US
 CURRENT APPLICATION NUMBER: US/09-282,277
 CURRENT FILING DATE: 1999-03-21
 EARLIER APPLICATION NUMBER: US 09/074,037
 EARLIER FILING DATE: 1998-05-06
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 1 LENGTH: 69
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide
 OTHER INFORMATION: used for cloning indolicidin
 US-09-282-277-1

Alignment Scores:
 Pred. No.: 0.376 Length: 69
 Score: 70.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 81.40% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-36 (1-12) x US-09-282-277-1 (1-69)

Qy 3 ArgTrpProTrpTrpProTrpArgArg 11
 Db 28 AAATGGCCCTGTCGGCTGGCCCGC 54

RESULT 4
 US-09-099-631A-11
 Sequence 11, Application US/09099631A
 Patent No. 6444615
 GENERAL INFORMATION:
 APPLICANT: Seisted, Michael E.
 APPLICANT: Osapay, Klara
 TITLE OF INVENTION: Crosslink-Stabilized Indolicidin Analogs

FILE REFERENCE: P-UC 3050
 CURRENT APPLICATION NUMBER: US/09/099,631A
 CURRENT FILING DATE: 1998-06-18
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 11 LENGTH: 211
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Construct
 US-09-099-631A-11

Alignment Scores:
 Pred. No.: 1.19 Length: 211
 Score: 70.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 81.40% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-36 (1-12) x US-09-099-631A-11 (1-211)

Qy 3 ArgTrpProTrpTrpProTrpArgArg 11
 Db ::::::::::::::::::::

Db 38 AAATGCCCTGGTGGCCGGTGGCGTGT 64

RESULT 5

US-09-416-481A-38

Sequence 38 Application US/09416481A

Patent No. 652455

GENERAL INFORMATION:

APPLICANT: Selsert, Michael E.

TITLE OF INVENTION: Indolicidin Analogs and Methods of Using Same

FILE REFERENCE: P-UC 3/794

CURRENT FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: US 09/076,227

PRIOR FILING DATE: 1998-05-12

NUMBER OF SEQ ID NOS.: 39

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 38

LENGTH: 211

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: CDS

LOCATION: (B) .. (196)

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: construct

US-09-416-481A-38

Alignment Scores:

Pred. No.:	1.19	Length:	211
Score:	70.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	88.89%	Mismatches:	0
Query Match:	81.40%	Indels:	0
DB:	4	Gaps:	0

US-09-444-281-36 (1-12) x US-09-259-741-5 (1-6446)

Qy 3 ArgTrpProTrpTrpProTrpArgArg 11

Db 6213 AAGGGCCUUGGGCAUAGGCCA 6239

RESULT 7

US-09-037-751-5

Sequence 5, Application US/09037751

GENERAL INFORMATION:

APPLICANT: GARGER, STEPHEN

APPLICANT: HOLTZ, R. BARRY

APPLICANT: MCCULLOCH, MICHAEL

APPLICANT: TURPIN, THOMAS

TITLE OF INVENTION: A PROCESS FOR ISOLATING AND

TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES

TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey & Simon

STREET: 1299 Pennsylvania Avenue N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004

CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

FILING DATE: 10-MAR-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 00801.0140.US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400

TELEX:

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 6446 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: Genomic RNA
 US-09-037-751-5

Alignment Scores:
 Pred. No.: 39.8 Length: 6446
 Score: 70.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 88.89% Mismatches: 0
 Query Match: 81.40% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-36 (1-12) x US-09-466-422-5 (1-6446)
 Qy 3 ArgTrpProTrpProTrpArg 11
 Db 6213 AAUGGCCCTGGGCCAUAGCGCGA 6239

RESULT 9
 US-09-252-991A-9269
 ; Sequence 9269, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; LENGTH: 1278
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-9269

Alignment Scores:
 Pred. No.: 47.8 Length: 1278
 Score: 63.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 73.26% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-36 (1-12) x US-09-252-991A-9269 (1-1278)
 Qy 4 TrpProTrpProTrpArg 10
 Db 885 TGGCCGTGGGCCCTGGCA 905

RESULT 10
 US-09-252-991A-9298/C
 ; Sequence 9298, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO. 9298
 ; LENGTH: 1362
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-9298

Alignment Scores:
 Pred. No.: 51 Length: 1362

Score: 63.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 73.26% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-36 (1-12) x US-09-252-991A-9298 (1-1362)

Qy 4 TDPproTTPproTTPArg 10
 Db 623 TGGCCCTGGCCCTGGGA 603

RESULT 11
 US-09-252-991A-9281 Application US/09252991A
 ; Sequence 9281, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/2322,991A
 CURRENT FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 981
 LENGTH: 1521
 TYPE: DNA
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-9281

Alignment Scores:
 Pred. No.: 57.1 Length: 1521
 Score: 63.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 73.26% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-36 (1-12) x US-09-252-991A-9281 (1-1521)

Qy 4 TDPproTTPproTTPArg 10
 Db 992 TGGCCCTGGCCCTGGGA 1012

RESULT 12
 US-09-793-035-6/c
 ; Sequence 6, Application US/08793035
 ; Patent No. 6011201

GENERAL INFORMATION:
 APPLICANT: Slatas, Antoni R.
 APPLICANT: White, Andrew
 APPLICANT: Chase, Dianne
 APPLICANT: Elborough, Keiran
 APPLICANT: Fentem, Phillip A.
 TITLE OF INVENTION: B-Ketoacyl ACP Reductase Genes From
 TITLE OF INVENTION: Brassica Napus
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: TX
 COUNTRY: US
 ZIP: 77210-4433
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/793,035
 FILING DATE: 28-JUL-1997
 CLASSIFICATION: 800
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB 9414622.2
 FILING DATE: 20-JUL-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: GB5/01678
 FILING DATE: 17-JUL-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Kammerer, Patricia A.
 REGISTRATION NUMBER: 29,775
 REFERENCE/DOCKET NUMBER: MOBT-132
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713.787.1400
 TELEFAX: 713.787.1440
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 758 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-793-035-6

Alignment Scores:
 Pred. No.: 47.3 Length: 758
 Score: 61.00 Matches: 7
 Percent Similarity: 88.89% Conservative: 1
 Best Local Similarity: 77.79% Mismatches: 1
 Query Match: 70.93% Indels: 0
 DB: 3 Gaps: 0

US-09-444-281-36 (1-12) x US-09-793-035-6 (1-758)

Qy 1 IleLeuArgTrpProTrpTrpProTrp 9
 Db 451 GTCCTGGCATGGAGGTGGCCATGG 425

RESULT 13
 US-09-118-554-59
 Sequence 59, Application US/09118554A
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Xu, Jiaochuan
 ; TITLE OF INVENTION: COMPOUNDS FOR THEIR USE
 ; FILE REFERENCE: 210121.45001
 ; CURRENT APPLICATION NUMBER: US/09/118-554A
 ; CURRENT FILING DATE: 1998-07-17
 ; EARLIER APPLICATION NUMBER: 08/118-554
 ; EARLIER FILING DATE: 1997-12-24
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 59
 ; LENGTH: 382
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-118-554-59

Alignment Scores:
 Pred. No.: 39.6 Length: 382
 Score: 59.00 Matches: 7
 Percent Similarity: 87.50% Conservative: 0
 Best Local Similarity: 87.50% Mismatches: 1
 Query Match: 68.60% Indels: 0
 DB: 4 Gaps: 0

US-09-444-281-36 (1-12) x US-09-118-554-59 (1-382)

Qy 2 LeuArgTrpProTrpTrpProTrp 9

Job time : 48.08 secs

Db 155 CTTGGCTGGCCTTGGTGGAGCTGG 178

RESULT 14

US-09-118-627-59

; Sequence 59, Application US/09118627A

; Patent No. 637951

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Xu, Jiangchun

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF BREAST CANCER

; TITLE OF INVENTION: AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.446C1

; CURRENT APPLICATION NUMBER: US/09/118,627A

; CURRENT FILING DATE: 1998-07-17

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: Fastseq for Windows Version 3.0

; SEQ ID NO 59

; LENGTH: 382

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-118-627-59

Alignment Scores:

Pred. No.:	39.6	Length:	382
Score:	59.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	68.60%	Indels:	0
DB:	4	Gaps:	0

US-09-444-281-36 (1-12) x US-09-118-627-59 (1-382)

Qy 2 LeuArgTrpProTrpTrpProTrp 9

Db 155 CTTGGCTGGCCTTGGTGGAGCTGG 178

RESULT 15

US-09-602-877A-59

; Sequence 59, Application US/09602877A

; Patent No. 6432707

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

; FILE REFERENCE: 210121.446C5

; CURRENT APPLICATION NUMBER: US/09/602,877A

; CURRENT FILING DATE: 2000-06-22

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: Fastseq for Windows Version 3.0

; SEQ ID NO 59

; LENGTH: 382

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-602-877A-59

Alignment Scores:

Pred. No.:	39.6	Length:	382
Score:	59.00	Matches:	7
Percent Similarity:	87.50%	Conservative:	0
Best Local Similarity:	87.50%	Mismatches:	1
Query Match:	68.60%	Indels:	0
DB:	4	Gaps:	0

US-09-444-281-36 (1-12) x US-09-602-877A-59 (1-382)

Qy 2 LeuArgTrpProTrpTrpProTrp 9

Db 155 CTTGGCTGGCCTTGGTGGAGCTGG 178

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 11, 2004, 14:35:33 ; search time 259.68 Seconds (without alignments)

209.334 Million cell updates/sec

Title: US-09-444-281-36

Perfect score: 86

Sequence: 1_1LRNFWWMRRK 12

Scoring table: BL2USM62

Xgapext 0.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

DelOp 6.0 , DelExt 7.0

Searched: 291586 seqs, 2264993651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Command line parameters:

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-Q-/cgn2_1/USP0_spool/US0944281/runat_07052004_171139_2611/app/query.fasta_1.398
-Ds=Published Applications NA -QFMT=rtsp -SUFFIX=rtsp -MINMATCH=0.1
-LOOPCFL0 -UNITS=bits -START=-END=-1 -MATRIXX=elosum62
-TRANS=human40 cdi -LIST=45 -DOCALIGN=ext -THR SCORE=0 -THR MAX=1.00
-TER_MIN=0 -ALIGN=5 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=15 -USER=0000000000 -USER=1_1_2704 @runat_07052004_171139_2611
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPEXT=0 -5
-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0 -5 -DELEXT=7
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Database : Published Applications NA:*

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- /cgn2_6_ptodata/2/pubpna/US06_NEW_PUB.seq:*
- /cgn2_6_ptodata/2/pubpna/US07_NEW_PUB.seq:*
- /cgn2_6_ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- /cgn2_6_ptodata/2/pubpna/US10_PUBCOMB.seq:*
- /cgn2_6_ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- /cgn2_6_ptodata/2/pubpna/US10_PUBCOMB.seq:*
- /cgn2_6_ptodata/2/pubpna/US60_NEW_PUB.seq:*
- /cgn2_6_ptodata/2/pubpna/US60_NEW_PUB.seq:*
- /cgn2_6_ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 32, Appl

Sequence 62, Appl

Sequence 29, Appl

Sequence 31, Appl

Sequence 30, Appl

Sequence 64, Appl

Sequence 65, Appl

Sequence 6, Appl

Sequence 60, Appl

Sequence 5, Appl

Sequence 25, Appl

Sequence 17, Appl

Sequence 19, Appl

Sequence 53929, A

Sequence 321717, A

Sequence 53929, A

Sequence 321717, A

Sequence 14181, A

Sequence 7766, Ap

Sequence 9716, Ap

Sequence 39517, A

Sequence 4600, Ap

Sequence 40578, A

Sequence 92875, A

Sequence 12845, A

Sequence 17644, A

Sequence 321, App

Sequence 157, App

Sequence 213, Ap

Sequence 22253, A

Sequence 30359, A

Sequence 1131, Ap

Sequence 17642, A

Sequence 27681, A

Sequence 14091, A

Sequence 4367, Ap

Sequence 2961, Ap

Sequence 12208, A

Sequence 12208, A

Sequence 59, Appl

ALIGNMENTS

RESULT 1

US-09-997-722-157

US-09-993-965-2138

US-10-425-599-92875

US-10-029-18845

US-10-424-599-17644

US-10-116-225-321

US-03-820-790-1

US-09-997-722-157

US-09-993-965-2138

US-10-425-599-92875

US-10-029-18845

US-10-424-599-17644

FEATURE:
 ; OTHER INFORMATION: Exemplary "template"
 US-10-395-896-32

Alignment Scores:
 Pred. No.: 0.00445 Length: 72
 Score: 86.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-10-395-896-32 (1-72)

Qy 1 IleLeuArgTrpProTrpProTrpArgArgLys 12
 Db 5 ATTCTGGTGGCCGGCGTGGCTGGCGTGGCAA 40

RESULT 2
 US-10-395-896-28
 ; Sequence 28, Application US/10395B96
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarna, Maria Marta
 ; APPLICANT: Chen, Yuchen
 ; APPLICANT: Cory, Robert
 ; APPLICANT: Brinkman, Jacqui
 ; APPLICANT: Cabralda, Jennifer
 ; APPLICANT: Melitskaya, Lubna
 ; APPLICANT: Suleiman, Dinar
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; FILE REFERENCE: 660081.421
 ; CURRENT APPLICATION NUMBER: US/10/395,896
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 28
 ; LENGTH: 121
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary "template"
 US-10-395-896-28

Alignment Scores:
 Pred. No.: 0.00712 Length: 121
 Score: 86.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-10-395-896-28 (1-121)

Qy 1 IleLeuArgTrpProTrpProTrpArgArgLys 12
 Db 48 ATTCTGGTGGCCGGCGTGGCTGGCGTGGCAA 83

RESULT 3
 US-10-395-896-62/c
 ; Sequence 62, Application US/10395B96
 ; Publication No. US/10395B96
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarna, Maria Marta
 ; APPLICANT: Chen, Yuchen
 ; APPLICANT: Cory, Robert
 ; APPLICANT: Brinkman, Jacqui
 ; APPLICANT: Cabralda, Jennifer
 ; APPLICANT: Melitskaya, Lubna
 ; APPLICANT: Suleiman, Dinar
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES
 ; FILE REFERENCE: 660081.421
 ; CURRENT APPLICATION NUMBER: US/10/395,896
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 62
 ; LENGTH: 121
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary "template"
 US-10-395-896-29

Alignment Scores:
 Pred. No.: 0.00723 Length: 123
 Score: 86.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-10-395-896-29 (1-123)

Qy 1 IleLeuArgTrpProTrpProTrpArgArgLys 12
 Db 26 ATTCTGGCTGGCCGGTGGCGTGGCGTGGCAA 61

RESULT 5
 US-10-395-896-31
 ; Sequence 31, Application US/10395B96
 ; Publication No. US/10395B96

GENERAL INFORMATION:
 ; APPLICANT: Guarina, Maria Marta
 ; APPLICANT: Chen, Yuchen
 ; APPLICANT: Cory, Robert
 ; APPLICANT: Brinkman, Jacqui
 ; APPLICANT: Cabralda, Jennifer
 ; APPLICANT: Metlitskaiia, Luba
 ; APPLICANT: Suleman, Dinar
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; PEPTIDES
 ; FILE REFERENCE: 660081.421
 ; CURRENT APPLICATION NUMBER: US/10/395, 896
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 31
 ; LENGTH: 139
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary "template"
 US-10-395-896-31

Alignment Scores:
 Pred. No.: 0.00807 Length: 139
 Score: 86.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-10-395-896-31 (1-139)

Qy 1 IleLeuArgTrpProTrpProTrpProTrpArgLys 12
 Db 41 ATTCGGTGGCGTGTGCGCTCCAAA 76

RESULT 6
 US-10-395-896-30

Sequence 30, Application US/10395896
 ; Publication No. US20030219854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarina, Maria Marta
 ; APPLICANT: Chen, Yuchen
 ; APPLICANT: Cory, Robert
 ; APPLICANT: Cabralda, Jennifer
 ; APPLICANT: Metlitskaiia, Luba
 ; APPLICANT: Suleman, Dinar
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; PEPTIDES
 ; FILE REFERENCE: 660081.421
 ; CURRENT APPLICATION NUMBER: US/10/395, 896
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 30
 ; LENGTH: 166
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Exemplary "template"
 US-10-395-896-30

Alignment Scores:
 Pred. No.: 0.00948 Length: 166
 Score: 86.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-10-395-896-30 (1-166)

Qy 1 IleLeuArgTrpProTrpProTrpProTrpArgLys 12
 Db 19 ATTCGGTGGCGTGTGCGCTCCAAA 54

RESULT 7
 US-10-395-896-64

Sequence 64, Application US/10395896
 ; Publication No. US20030219854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarina, Maria Marta
 ; APPLICANT: Chen, Yuchen
 ; APPLICANT: Cory, Robert
 ; APPLICANT: Brinkman, Jacqui
 ; APPLICANT: Cabralda, Jennifer
 ; APPLICANT: Metlitskaiia, Luba
 ; APPLICANT: Suleman, Dinar
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; PEPTIDES
 ; FILE REFERENCE: 660081.421
 ; CURRENT APPLICATION NUMBER: US/10/395, 896
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 64

Alignment Scores:
 Pred. No.: 0.0278 Length: 114
 Score: 81.00 Matches: 11
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 94.19% Indels: 0
 DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-10-395-896-64 (1-114)

Qy 1 IleLeuArgTrpProTrpProTrpProTrpArgLys 11
 Db 30 ATTCGGTGGCGTGTGCGCTCCAAA 62

RESULT 8
 US-10-395-896-65/c

Sequence 65, Application US/10395896
 ; Publication No. US20030219854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Guarina, Maria Marta
 ; APPLICANT: Chen, Yuchen
 ; APPLICANT: Cory, Robert
 ; APPLICANT: Brinkman, Jacqui
 ; APPLICANT: Cabralda, Jennifer
 ; APPLICANT: Metlitskaiia, Luba
 ; APPLICANT: Suleman, Dinar
 ; TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
 ; PEPTIDES
 ; FILE REFERENCE: 660081.421
 ; CURRENT APPLICATION NUMBER: US/10/395, 896
 ; CURRENT FILING DATE: 2003-03-21
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 65

Alignment Scores:
 Pred. No.: 0.00948 Length: 166
 Score: 86.00 Matches: 12
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-10-395-896-65 (1-166)

US-10-395-896-65

Alignment Scores:
Pred. No.: 0.0278 Length: 114
Score: 81.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.19% Indels: 0
DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-10-395-896-65 (1-114)

Qy 1 IleLeuGluGTPProTrpTrpProTrpArgArg 11
Db 85 ArgTrpGCTTGGCCCTGGTGGCGCTCGCG 53

RESULT 9
US-09-909-652-6

; Sequence 6, Application US/09909652
; Patent No. US20020025537A1

; GENERAL INFORMATION:
; APPLICANT: Kairos Scientific, Inc.
; APPLICANT: Bylina, Edward J.
; APPLICANT: Coleman, William J.
; APPLICANT: Youvan, Douglas C.
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
; AND SCREENING COMPOUNDS THAT AFFECT CELL VIABILITY
; FILE REFERENCE: 22346-7001
; CURRENT APPLICATION NUMBER: US/09/909,652
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/219,179
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding ubiquitin indolicidin fusion
US-09-909-652-6

Alignment Scores:
Pred. No.: 0.0278 Length: 114
Score: 81.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 94.19% Indels: 0
DB: 16 Gaps: 0

US-09-444-281-36 (1-12) x US-09-909-652-6 (1-68)

Qy 2 LeuGluGTPProTrpTrpProTrpArgArg 11
Db 28 TTGAAATGGCTTGGCCCTGGCGTCGC 57

RESULT 10
US-10-076-816-60

; Sequence 60, Application US/10076816
; GENERAL INFORMATION: Feed Additive Compositions and Methods
; APPLICANT: Rodriguez, Raymond
; APPLICANT: Hsieh, Frank E.
; TITLE OF INVENTION: Feed Additive Compositions and Methods
; FILE REFERENCE: 50665-8021.US00
; CURRENT APPLICATION NUMBER: US/10/076,816
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/269,188
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/847,232
; PRIOR FILING DATE: 2001-05-02

; PRIORITY: US 60/266,929
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: US 60/201,182
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 60
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Bos taurus
; US-10-076-816-60

Alignment Scores:
Pred. No.: 2.61 Length: 550
Score: 70.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 81.40% Indels: 0
DB: 15 Gaps: 0

US-09-444-281-36 (1-12) x US-10-076-816-60 (1-550)

Qy 3 ArgTrpProTrpTrpProTrpArgArg 11
Db 415 AAATGCCATGGGCCCTGGCAGA 441

RESULT 11
US-09-962-527-5

; Sequence 5, Application US/09962527
; Publication No. US20030049813A1
; GENERAL INFORMATION:
; APPLICANT: GANGER, STEPHEN
; APPLICANT: HOTZ, R. BARRY
; APPLICANT: McCULLOCH, MICHAEL
; APPLICANT: TUPPER, THOMAS
; TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
; PURIFYING VIRUS SOLUBLE PROTEINS AND PEPTIDES
; NUMBER OF SEQUENCES: 5
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/09/962,527
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P
; TELE: <Unknown>
; FILING DATE: 24-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/037,751
; FILING DATE: 10-march-1998
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-109
; TELEFAX: 650-463-8430
; INFORMATION FOR SEQ ID NO: 5:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: Genomic RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

US-09-962-527-5

Alignment Scores:
Pred. No.: 24.00 Length: 6446
Score: 70.00 Matches: 8
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 81.40% Indels: 0
DB: 10 Gaps: 0

US-09-444-281-36 (1-12) x US-09-962-527-5 (1-6446)

Qy 3 ArgTrpProTrpProTrpProTrpArg 11
Db 6213 ArgGCGCCUGGUGGCAUGGCCGGA 6239

RESULT 12
US-10-252-773-25
; Sequence 25, Application US/10252773
; Publication No. US2003013138A1
; GENERAL INFORMATION:
; APPLICANT: EVERETT, NICHOLAS P.
; APPLICANT: LI, QUNGSUN
; APPLICANT: LAWRENCE, CHRISTOPHER
; APPLICANT: DAVIES, MAELOH H.
; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
; TITLE OF INVENTION: DEGRADATION
; FILE REFERENCE: INTERLINK 3.0-003
; CURRENT APPLICATION NUMBER: US/10/252,773
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/105,373
; PRIOR FILING DATE: 1998-10-10
; PRIOR APPLICATION NUMBER: 60/106,573
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 25

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA PCRIL
; OTHER INFORMATION: construct
US-10-252-773-25

Alignment Scores:
Pred. No.: 2.53 Length: 207
Score: 67.00 Matches: 8
Percent Similarity: 90.00% Conservative: 1
Best Local Similarity: 80.00% Mismatches: 1
Query Match: 77.91% Indels: 0
DB: 15 Gaps: 0

US-09-444-281-36 (1-12) x US-10-252-773-25 (1-207)

Qy 1 IleLeuGArgTrpProTrpProTrpArg 10
Db 163 ATTAGGAGATGGCTGGCTGGCTGGAA 192

RESULT 13
US-10-252-773-15
; Sequence 15, Application US/10252773
; Publication No. US2003013138A1
; GENERAL INFORMATION:
; APPLICANT: EVERETT, NICHOLAS P.
; APPLICANT: LI, QUNGSUN
; APPLICANT: LAWRENCE, CHRISTOPHER
; APPLICANT: DAVIES, MAELOH H.
; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
; TITLE OF INVENTION: DEGRADATION
; FILE REFERENCE: INTERLINK 3.0-003
; CURRENT APPLICATION NUMBER: US/10/252,773

CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/106,373
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106,573
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 15
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-252-773-15

Alignment Scores:
Pred. No.: 0.983 Length: 39
Score: 65.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 75.58% Indels: 0
DB: 15 Gaps: 0

US-09-444-281-36 (1-12) x US-10-252-773-15 (1-39)

Qy 3 ArgTrpProTrpProTrpProTrpArg 10
Db 4 AGATGGCTGGCTGGCTGGAA 27

RESULT 14
US-10-252-773-17/C
; Sequence 17 Application US/10252773
; Publication No. US2003013138A1
; GENERAL INFORMATION:
; APPLICANT: EVERETT, NICHOLAS P.
; APPLICANT: LI, QUNGSUN
; APPLICANT: LAWRENCE, CHRISTOPHER
; APPLICANT: DAVIES, MAELOH H.
; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
; TITLE OF INVENTION: DEGRADATION
; FILE REFERENCE: INTERLINK 3.0-003
; CURRENT APPLICATION NUMBER: US/10/252,773
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: 60/106,373
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106,573
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 17
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-252-773-17

Alignment Scores:
Pred. No.: 1.3 Length: 53
Score: 65.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 75.58% Indels: 0
DB: 15 Gaps: 0

US-09-444-281-36 (1-12) x US-10-252-773-17 (1-53)

Qy 3 ArgTrpProTrpProTrpProTrpArg 10
Db 50 AGATGGCTGGCTGGCTGGAA 27

RESULT 15

US-10-252-773-19/c
 ; Sequence 19, Application US/10252773
 ; Publication No. US0030131383A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EVERETT, NICHOLAS P.
 ; APPLICANT: LI, QUNIGSHUN
 ; APPLICANT: LAWRENCE, CHRISTOPHER
 ; APPLICANT: DAVIES, MAELOR H.
 ; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
 ; TITLE OF INVENTION: DEGRADATION
 ; FILE REFERENCE: INTERLINK 3.0-003
 ; CURRENT APPLICATION NUMBER: US/10/252,773
 ; CURRENT FILING DATE: 2002-09-23
 ; PRIORITY NUMBER: 60/106,373
 ; PRIORITY FILING DATE: 1998-10-30
 ; PRIORITY APPLICATION NUMBER: 60/106,573
 ; PRIORITY FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 19
 ; LENGTH: 54
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:
 ; OTHER INFORMATION: Oligonucleotide
 US-10-252-773-19

Alignment Scores:
 Pred. No.: 1.32 Length: 54
 Score: 65.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 87.50% Mismatches: 0
 Query Match: 75.58% Indels: 0
 DB: 15 Gaps: 0
 US-09-444-281-36 (1-12) x US-10-252-773-19 (1-54)
 Qy 3 ArgrpDproTrpTrpTrpTrpArg 10
 Db 51 AGATGGCTTGCTGCTGAA 28

Search completed: May 11, 2004, 17:07:35
 Job time : 262.68 secs

AUTHORS Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D.

TITLE An EST database from well-watered loblolly pine (*Pinus taeda*) roots

JOURNAL Unpublished

COMMENT Other ESTs: RTW93_23_A01_b1_A022

CONTACT Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology,
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Te: 706 542 1860
Fax: 706 583 0210
Email: mpratt@uga.edu

RNA prepared and library constructed by Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are present as their reverse complement and have been trimmed to exclude polyA.

Seq Primer: JENRAY (CAGGAAAGCTATGACCC).

Location/Qualifiers

1. . 522

/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLOONES"
/db_xref="taxon:3352"

/clone=RTW93_23_A01_A022"
/lab_host="DH10B-T1 Phage-resistant E. coli"
/lab="Well-watered loblolly pine roots WW3"
/note="vector: pSL180; Site 1: EcoRI; Site 2: XbaI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Insects excised with EcoRI (5' end) and XbaI (3' end)."

ORIGIN

Alignment Scores:
Pred. No.: 203
Score: 75.00
Percent Similarity: 100.00%
Best Local Similarity: 87.21%
Query Match: 14
DB: 287

US-09-444-281-36 (1-12) x CF479395 (1-522)

QY 3 ArgTrpProTrpProTrpArgGly 12

Db 287 AGGGCCCTGCTGGCCGAGG 316

RESULT 2

LOCUS AUI98144/c

DEFINITION AUI98144 Rice Green shoot *Oryza sativa* (japonica cultivar-group) cDNA clone S15951, mRNA sequence.

ACCESSION AUI98144

VERSION AUI98144.1

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group) Spermatophyta; Magnoliophyta; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Monocots; Poales; Poaceae; Ehrhartioidae; Orzyeae; Orzya.

REFERENCE Sasaki,T. and Yamamoto,K.

AUTHORS Sasaki,T. and Yamamoto,K.

TITLE Rice cDNA from green shoot (2001)

JOURNAL Unpublished

COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki

305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@brr.affrc.go.jp, URL:<http://rgp.dna.affrc.go.jp/>

FEATURES

source

PROJECT = 'RGP'
Location/Qualifiers

1. . 446

/organism="Oryza sativa" (japonica cultivar-group)
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="S15951"
/clone.lib="Rice green shoot"
/note="Green shoot (8 days old)"

ORIGIN

Alignment Scores:
Pred. No.: 687
Score: 69.00
Percent Similarity: 90.00%
Best Local Similarity: 80.00%
Query Match: 80.23%
DB: 9

US-09-444-281-36 (1-12) x AUI98144 (1-446)

QY 3 ArgTrpProTrpProTrpArgGly 12

Db 348 CGTGGCCCTGGCCCTGGACGGGGGG 319

RESULT 3

LOCUS AUI98162/c

DEFINITION AUI98162 Rice green shoot *Oryza sativa* (japonica cultivar-group) cDNA clone S16019, mRNA sequence.

ACCESSION AUI98162

VERSION AUI98162.1

KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group) Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioidae; Orzyeae; Orzya.

REFERENCE 1 (bases 1 to 448)

AUTHORS Sasaki,T. and Yamamoto,K.

TITLE Rice cDNA from green shoot (2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki

305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@brr.affrc.go.jp, URL:<http://rgp.dna.affrc.go.jp/>

FEATURES

source

PROJECT = 'RGP'
Location/Qualifiers

1. . 446

/organism="Oryza sativa" (japonica cultivar-group)
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="S16019"
/clone.lib="Rice green shoot (8 days old)"

ORIGIN

Alignment Scores:
Pred. No.: 691
Score: 69.00
Percent Similarity: 90.00%
Best Local Similarity: 80.00%
Query Match: 80.23%
DB: 9

US-09-444-281-36 (1-12) x AU198162 (1-448)	VERSION	CF326444.1	GI:33801141
Qy 3 ArgTrpProTrpProTrpArgArgLys 12	KEYWORDS		
Db 311 CGCTGGCTTGTGGCCCTGACGGCG 282	SOURCE	Oryza sativa	
RESULT 4	ORGANISM	Oryza sativa	
CP326637/c	REFERENCE	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.	
LOCUS JMT1-06-J20-91 AtJMT-overexpressing transgenic rice lambda phage	AUTHORS		
DEFINITION cDNA library (JMT1) Oryza sativa cDNA clone JMT1-06-J20, mRNA sequence.	TITLE		
ACCESSION CR226637	JOURNAL		
VERSION CR226637.1	COMMENT	Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)	
KEYWORDS EST	CONTACT	Nahm B.H.	
ORGANISM Oryza sativa	GENOMICS AND GENETICS INSTITUTE	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University	
SOURCE	EMAIL	bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.	
FEATURES	LOCATION/QUALIFIERS	Yongin, Kyonggi, Korea	
SOURCE	1. 539		
REFERENCE	/organism="Oryza sativa"		
AUTHORS	/mol_type="mRNA"		
LOCUS	/cultivar="Nackdong"		
DEFINITION	/db_xref="Taxon:4530"		
JOURNAL	/clone="JMT1-06-B08"		
COMMENT	/issue_type="leaf"		
CONTRACT	/dev_stage="14 days after germination"		
GENOMICS AND GENETICS INSTITUTE	/dev_host="E. coli SOLR"		
YONGIN, KYONGGI, KOREA	/clone_lib="ATMt-overexpressing transgenic rice lambda phage cDNA library (JMT1)"		
TEL: 82 31 321 6193	/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XbaI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'		
FAX: 82 31 321 6355	/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XbaI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'		
EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.	/note="Vector: pBluescript SK(+); Site 1: EcoRI and 3' end with XbaI site. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."		
FEATURES	ORIGIN		
SOURCE	1. 539		
ORGANISM /organism="Oryza sativa"	ALIGNMENT SCORES:		
KEYWORDS /mol_type="mRNA"	PRED. NO.:	881	Length: 550
LOCUS /cultivar="Nackdong"	SCORE:	69.00	Matches: 8
DEFINITION /db_xref="Taxon:4530"	PERCENT SIMILARITY:	90.00%	Conservative: 1
JOURNAL /tissue_type="leaf"	BEST LOCAL SIMILARITY:	80.00%	Mismatches: 1
COMMENT /dev_stage="14 days after germination"	QUERY MATCH:	80/23%	INDELS: 0
CONTRACT /lab_host="E. coli SOLR"	DB:	14	GAPS: 0
GENOMICS AND GENETICS INSTITUTE /clone_lib="AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"	US-09-444-281-36 (1-12) x CF326444 (1-550)		
YONGIN, KYONGGI, KOREA /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XbaI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'	QY 3 ArgTrpProTrpProTrpArgArgLys 12		
TEL: 82 31 321 6193	DB 352 CGCTGCCTGATGCCCTGAGCGCG 323		
FAX: 82 31 321 6355	RESULT 6		
EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.	CF225873/c	CF325873	CF325873/c
FEATURES	LOCUS	LOCUS	LOCUS
SOURCE	DEFINITION	DEFINITION	DEFINITION
ORGANISM	ACCESSION	ACCESSION	ACCESSION
KEYWORDS	VERSION	VERSION	VERSION
SEQUENCE	SOURCE	SOURCE	SOURCE
CONTACT	ORIGIN	ORIGIN	ORIGIN
GENOMICS AND GENETICS INSTITUTE	ORGYA SATIVA	ORGYA SATIVA	ORGYA SATIVA
YONGIN, KYONGGI, KOREA	SPERMATOPHYTA	SPERMATOPHYTA	SPERMATOPHYTA
TEL: 82 31 321 6193	ELHARTOIDEAE	ELHARTOIDEAE	ELHARTOIDEAE
FAX: 82 31 321 6355	ORYZEAE	ORYZEAE	ORYZEAE
EMAIL: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.	UNPUBLISHED (2003)	UNPUBLISHED (2003)	UNPUBLISHED (2003)
COMMENT	CONTACT	CONTACT	CONTACT
CONTRACT	GENOMICS AND GENETICS INSTITUTE	GENOMICS AND GENETICS INSTITUTE	GENOMICS AND GENETICS INSTITUTE
GENOMICS AND GENETICS INSTITUTE	GREENGENE BIOTECH INC.	GREENGENE BIOTECH INC.	GREENGENE BIOTECH INC.

of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahn@gsbiol.com, bhnahn@bio.myongji.ac.kr.

FEATURES
 Source
 Location/Qualifiers
 1. .559
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4510"
 /clone="JMTI-04-H99"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E. coli SOLR"
 /clone_lib="ATMT-overexpressing transgenic rice lambda phage cDNA library (JMTI)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XbaI; cDNA was inserted into Lambda Uni-ZAP XR vector at 5', end with EcoRI and 3', end with XbaI site. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

.ORIGIN

Alignment Scores:
 Prd. No.: 898 Length: 559
 Score: 69.00 Matches: 8
 Percent Similarity: 90.00% Conservative: 1
 Best Local Similarity: 90.00%
 Query Match: 80.23%
 DB: 14 Gaps: 0

US-09-444-281-36 (1-12) x AU082117 (1-578)

QY 3 ArgTrpProTrpProTrpProTrpArgLys 12
 Db 345 CGCTGGCTTGCCCTGACGGCG 316

RESULT 8

CF326279/c
 LOCUS JMTI-05-K03.g1 At JMTI-overexpressing transgenic rice lambda phage cDNA library (JMTI) Oryza sativa cDNA clone JMTI-05-K03, mRNA sequence.

ACCESSION CF326279
 VERSION CF326279.1
 GI:33800815
 EST.
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bokaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 595)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Unpublished (2003)
 Contact: Nahm B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs.
 JOURNAL
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahn@gsbiol.com, bhnahn@bio.myongji.ac.kr.

FEATURES
 Source
 Location/Qualifiers
 1. .555
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMTI-05-K03"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E. coli SOLR"
 /clone_lib="ATMT-overexpressing transgenic rice lambda phage cDNA library (JMTI)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XbaI; cDNA was inserted into Lambda Uni-ZAP XR vector at 5', end with EcoRI and 3', end with XbaI site. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

DEFINITION Rice panicle at ripening stage Oryza sativa (japonica cultivar-group) cDNA clone E11611, mRNA sequence.

ACCESSION AU082117
 VERSION AU082117.1
 GI:6727452
 KEYWORDS Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (bases 1 to 578)
 AUTHORS Sasaki,T. and Yamamoto,K.
 TITLE Rice cDNA from panicle at ripening stage (2000)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takuji Sasaki
 National Institute of Agrobiological Resources
 305-8602, Japan
 Tel: 81-298-38-7441
 Email: tssasaki@abfaffrc.go.jp, URL: http://r9p.dna.affrc.go.jp/
 PROJECT = RGP

FEATURES
 Source
 Location/Qualifiers
 1. .578
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="E11611"
 /dev_stage="ripening stage"
 /clone_lib="Rice panicle at ripening stage"
 /note="Organ: panicle; Rice cDNA from panicle at ripening stage"

DEFINITION At JMTI-overexpressing transgenic rice lambda phage cDNA library (JMTI) Oryza sativa cDNA clone JMTI-05-K03, mRNA sequence.

ACCESSION CF326279
 VERSION CF326279.1
 GI:33800815
 EST.
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bokaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 595)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Unpublished (2003)
 Contact: Nahm B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs.
 JOURNAL
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahn@gsbiol.com, bhnahn@bio.myongji.ac.kr.

DEFINITION At JMTI-overexpressing transgenic rice lambda phage cDNA library (JMTI) Oryza sativa cDNA clone JMTI-05-K03, mRNA sequence.

ACCESSION CF326279
 VERSION CF326279.1
 GI:33800815
 EST.
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 595)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Unpublished (2003)
 Contact: Nahm B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs.
 JOURNAL
 COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahn@gsbiol.com, bhnahn@bio.myongji.ac.kr.

Db	322	ccctgccttgcgtggccctggacggcgccg	293	ORGANISM	Mus musculus
RESULT	9	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		REFERENCE	1 (bases 1 to 742)
LOCUS	CB681162/c	661 bp	mRNA	AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
DEFINITION	OSJNEf07B03_f_ OSJNEf07B03_f_ Oryza sativa (japonica cultivar-group) cDNA	linear	EST	TITLE	Unpublished (1999)
ACCESSION	CB681162	clone OSJNEf07B03 5'	mRNA sequence.	JOURNAL	
VERSION	EST.			COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsbs@mail.nih.gov
KEYWORD	Orzya sativa (japonica cultivar-group)				Tissue Procurement: Gilbert Smith, Ph.D.
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				cDNA Library Preparation: Life Technologies, Inc.
REFERENCE	1 (bases 1 to 661)				cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)
AUTHORS	Jantsariyarat, C., Iu, G., Gowda, M., Hatfield, J., Zhou, B., Nazir, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.				DNA Sequencing by: Incyte Genomics, Inc.
TITLE	Large scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea				Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:
JOURNAL	Unpublished (2003)				http://image.llnl.gov
COMMENT	Contact: Rod Wing				Plate: LILM11946 row: h column: 05
VERSION	EST.				Location/Qualifiers
KEYWORD	Orzya sativa (japonica cultivar-group)				1. .742
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				/organism="Mus musculus"
FEATURES	source				/mol_type="mRNA"
COMMENT	Unpublished (2003)				/strain="FVB/N-3"
VERSION	EST.				/db_xref="taxon:10090"
KEYWORD	Orzya sativa (japonica cultivar-group)				/clone="IMAGE:5371528"
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				/tissue_type="tumor, biopsy sample"
FEATURES	source				/dev_stage="5 months"
COMMENT	Unpublished (2003)				/lab_host="DH10B"
VERSION	EST.				/clone_lib="NCI CGAP Mamm2"
KEYWORD	Orzya sativa (japonica cultivar-group)				/note="Organ: mammary; Vector: pCMW-SPORT6; Site: 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
FEATURES	source				ORIGIN
COMMENT	Unpublished (2003)				
VERSION	EST.				Alignment Scores:
KEYWORD	Orzya sativa (japonica cultivar-group)				Pred. No. : 1.26e+03
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				Score: 69.00
FEATURES	source				Percent Similarity: 90.00%
COMMENT	Unpublished (2003)				Best Local Similarity: 80.00%
VERSION	EST.				Query Match: 80.23%
KEYWORD	Orzya sativa (japonica cultivar-group)				DB: 12
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				Indels: 0
FEATURES	source				Gaps: 0
COMMENT	Unpublished (2003)				US-09-444-281-36 (1-12) x BI698060 (1-742)
VERSION	EST.				QY 3 ArgTrpProTrpTrpProTrpArgGly 12
KEYWORD	Orzya sativa (japonica cultivar-group)				Db 222 AGGGCCCTGTGGCCCTGAGGTCGG 251
FEATURES	source				RESULT 11
COMMENT	Unpublished (2003)				BQ931041
VERSION	EST.				LOCUS BQ931041
KEYWORD	Orzya sativa (japonica cultivar-group)				DEFINITION AGENCODE 8933817 NCI CGAP Mam2 Mus musculus mRNA clone
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				IMAGE:6487249 5', mRNA sequence.
FEATURES	source				ACCESSION BQ931041
COMMENT	Unpublished (2003)				VERSION BQ931041.1
VERSION	EST.				KEYWORDS EST.
KEYWORD	Orzya sativa (japonica cultivar-group)				SOURCE Mus musculus (house mouse)
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				ORGANISM Mus musculus
FEATURES	source				REFERENCE NIH-MGC http://mhc.nih.gov/
COMMENT	Unpublished (2003)				AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
VERSION	EST.				TITLE Unpublished (1999)
KEYWORD	Orzya sativa (japonica cultivar-group)				JOURNAL Contact: Robert Strausberg, Ph.D. Email: cgsbs@mail.nih.gov
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				Tissue Procurement: Life Technologies, Inc.
FEATURES	source				cDNA Library Preparation: The I.M.A.G.E. Consortium (LILN)
COMMENT	Unpublished (2003)				DNA Sequencing by: Agencourt Bioscience Corporation
VERSION	EST.				Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at:
KEYWORD	Orzya sativa (japonica cultivar-group)				http://image.llnl.gov
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
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SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
FEATURES	source				
COMMENT	Unpublished (2003)				
VERSION	EST.				
KEYWORD	Orzya sativa (japonica cultivar-group)				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoli				

http://image.llnl.gov
Plate: LIAM14037 Row: C Column: 10
High quality sequence stop: 539.

FEATURES
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Location/Qualifiers
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/clone_idb="NCI CGAP Man2"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site: 1; Sali"
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH¹

ORIGIN
Alignment Scores:
Pred. No.: 1.68e-03
Score: 67.00+
Percent Similarity: 90.00%
Best Local Similarity: 80.00%
Query Match: 80.23%
DB: 13

US-09-444-281-36 (1-12) x BQ931041 (1-946)

Qy 3 ArgTrpProTrpProTrpArgGly 12
Db 76 AGGTGGCTTGTTGCCCTGGGTCGG 105

RESULT 12
BQ877964
LOCUS BQ877964 959 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT 8712713 NIH_MGC_129 Mus musculus cDNA clone IMAGE:630797
5'. mRNA Sequence.
ACCESSION BQ877964
VERSION BQ877964.1 GI:22269972
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus (house mouse)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 959)
REFERENCE NIH-MGC http://mcg.ncbi.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgs@csra-mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNNL at:
http://image.llnl.gov
Plate: LIAM13732 row: m column: 23
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/clone="IMAGE:6310462"
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/clone_idb="NIH_MGC_129"
/note="Organ: olfactory epithelium; Vector: PCMV-SPORT6.1;
Site: 1; BcRV; Site: 2; NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."
ORIGIN
Alignment Scores:
Pred. No.: 1.76e-03
Score: 69.00+
Percent Similarity: 90.00%
Best Local Similarity: 80.00%
Query Match: 80.23%
DB: 13

US-09-444-281-36 (1-12) x BQ715181 (1-984)

Qy 3 ArgTrpProTrpProTrpArgGly 12
Db 415 AGGNGGCCCTGGTGGCCCTGGGTCGG 444

RESULT 14	BQ715516	1011 bp	mRNA	linear	EST 16-III-2002
LOCUS	BQ715516	1011 bp	mRNA	linear	EST 16-III-2002
DEFINITION	AGENCOURT 8294996 NIH MGC_129 Mus musculus cDNA clone IMAGE:63094705', mRNA sequence.				
ACCESSION	BQ715516				
KEYWORDS	EST. BQ715516.1 GI:21854415				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus. 1 (bases 1 to 1011)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished. (1998)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsobs@mail.nih.gov				
FEATURES	Tissue Preparation: Susan L. Sullivan, PhD. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)				
Source	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNNL at: http://image.llnl.gov Plate: L1AM13730 row: d column: 15				
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	/lab_host="DHLOB (phage-resistant)"				
	/clone_id="NIH MGC_129"				
	/note="Organ: olfactory epithelium; Vector: PCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."				
ORIGIN	Alignment Scores:				
	Pred. No. : 1.8e+03	Length: 1011			
	Score: 69.00	Matches: 8			
	Percent Similarity: 90.00%	Conservative: 1			
	Best Local Similarity: 80.00%	Mismatches: 1			
	Query Match: 80.23%	Indels: 0			
	DB: 13	Gaps: 0			
Qy	3 ArgTrpProTrpProTrpArgArgly 12				
Db	198 AGTGGCTTGTGGCTGAGTCAGGG 227				
RESULT 15	BC051074	2675 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	BC051074	2675 bp	mRNA	linear	HTC 19-NOV-2003
DEFINITION	Mus musculus elastin, mRNA (cDNA clone IMAGE:6390348), with apparent retained intron.				
ACCESSION	BC051074				
VERSION	BC051074.1 GI:30048428				
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 2675)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,				

DEFINITION	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Logueillo, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malik, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fay, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grinow, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smajus, D.E., Scherzer, A., Schein, J.B., Jones, S.J., and Marrs, M.A.				
ACCESSION	BQ715516				
KEYWORDS	EST. BQ715516.1 GI:21854415				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.				
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
COMMENT	Unpublished. (1998)				
FEATURES	Tissue Preparation: Susan L. Sullivan, PhD. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)				
Source	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNNL at: http://image.llnl.gov Plate: L1AM13730 row: d column: 15				
	High quality sequence stop: 554.				
	Location/Qualifiers:				
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	/lab_host="DHLOB (phage-resistant)"				
	/clone_id="NIH MGC_129"				
	/note="Organ: olfactory epithelium; Vector: PCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."				
ORIGIN	Alignment Scores:				
	Pred. No. : 1.8e+03				
	Score: 69.00				
	Percent Similarity: 90.00%				
	Best Local Similarity: 80.00%				
	Query Match: 80.23%				
	DB: 13				
Qy	US-09-444-281-36 (1-12) x BQ715516 (1-1011)				
Db	3 ArgTrpProTrpProTrpArgArgly 12				
	198 AGTGGCTTGTGGCTGAGTCAGGG 227				
RESULT 15	BC051074	2675 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	BC051074	2675 bp	mRNA	linear	HTC 19-NOV-2003
DEFINITION	Mus musculus elastin, mRNA (cDNA clone IMAGE:6390348), with apparent retained intron.				
ACCESSION	BC051074				
VERSION	BC051074.1 GI:30048428				
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 2675)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,				

DEFINITION	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Logueillo, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malik, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fay, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grinow, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smajus, D.E., Scherzer, A., Schein, J.B., Jones, S.J., and Marrs, M.A.				
ACCESSION	BQ715516				
KEYWORDS	EST. BQ715516.1 GI:21854415				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.				
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
COMMENT	Unpublished. (1998)				
FEATURES	Tissue Preparation: Susan L. Sullivan, PhD. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)				
Source	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNNL at: http://image.llnl.gov Plate: L1AM13730 row: d column: 15				
	High quality sequence stop: 554.				
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	/lab_host="DHLOB (phage-resistant)"				
	/clone_id="NIH MGC_129"				
	/note="Organ: olfactory epithelium; Vector: PCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."				
ORIGIN	Alignment Scores:				
	Pred. No. : 1.8e+03				
	Score: 69.00				
	Percent Similarity: 90.00%				
	Best Local Similarity: 80.00%				
	Query Match: 80.23%				
	DB: 13				
Qy	US-09-444-281-36 (1-12) x BQ715516 (1-1011)				
Db	3 ArgTrpProTrpProTrpArgArgly 12				
	198 AGTGGCTTGTGGCTGAGTCAGGG 227				
RESULT 15	BC051074	2675 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	BC051074	2675 bp	mRNA	linear	HTC 19-NOV-2003
DEFINITION	Mus musculus elastin, mRNA (cDNA clone IMAGE:6390348), with apparent retained intron.				
ACCESSION	BC051074				
VERSION	BC051074.1 GI:30048428				
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 2675)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,				

DEFINITION	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Logueillo, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malik, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fay, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grinow, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smajus, D.E., Scherzer, A., Schein, J.B., Jones, S.J., and Marrs, M.A.				
ACCESSION	BQ715516				
KEYWORDS	EST. BQ715516.1 GI:21854415				
ORGANISM	Mus musculus (house mouse)				
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.				
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
COMMENT	Unpublished. (1998)				
FEATURES	Tissue Preparation: Susan L. Sullivan, PhD. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)				
Source	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNNL at: http://image.llnl.gov Plate: L1AM13730 row: d column: 15				
	High quality sequence stop: 554.				
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	1. 1011 "Mus musculus"				
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	/note="Organ: olfactory epithelium; Vector: PCMV-SPORT6"				
ORIGIN	Alignment Scores:				
	Pred. No. : 1.8e+03				
	Score: 69.00				
	Percent Similarity: 90.00%				
	Best Local Similarity: 80.00%				
	Query Match: 80.23%				
	DB: 13				
Qy	US-09-444-281-36 (1-12) x BQ715516 (1-1011)				
Db	3 ArgTrpProTrpProTrpArgArgly 12				
	198 AGTGGCTTGTGGCTGAGTCAGGG 227				
RESULT 15	BC051074	2675 bp	mRNA	linear	HTC 19-NOV-2003
LOCUS	BC051074	2675 bp	mRNA	linear	HTC 19-NOV-2003
DEFINITION	Mus musculus elastin, mRNA (cDNA clone IMAGE:6390348), with apparent retained intron.				
ACCESSION	BC051074				
VERSION	BC051074.1 GI:30048428				
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 2675)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Sherman, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,				

DEFINITION	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Logueillo, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malik, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fay, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grinow, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smajus, D.E., Scherzer, A., Schein, J.B., Jones, S.J., and Marrs, M.A.
ACCESSION	BQ715516
KEYWORDS	EST. BQ715516.1 GI:21854415
ORGANISM	Mus musculus (house mouse)
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
COMMENT	Unpublished. (1998)
FEATURES	Tissue Preparation: Susan L. Sullivan, PhD. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNNL)
Source	DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNNL at: http://image.llnl.gov Plate: L1AM13730 row: d column: 15
	High quality sequence stop: 554.
	Location/Qualifiers:
	1. 1011 "Mus musculus"
	/organism="Mus musculus"
	/mol_type="mRNA"
	/db_xref="TAXON:10090"
	/clone=IMAGE:63094705
	/lab_host="DHLOB (phage-resistant)"
	/clone_id="NIH MGC_129"
	/note="Organ: olfactory epithelium; Vector: PCMV-SPORT6"
ORIGIN	Alignment Scores:
	Pred. No. : 1.8e+03
	Score: 69.00
	Percent Similarity: 90.00%
	Best Local Similarity: 80.00%
	Query Match: 80.23%
	DB: 13
Qy	US-09-4

US-09-444-281-36 (1-12) x BC051074 (1-2675)
QY 3 ArgTrpProTrpProTrpArgArgLys 12
Db 1112 AGTGGCCCTTGCTGCCCTGGAGGTCGG 1141

Search completed: May 11, 2004, 16:56:35
Job time : 1591.8 secs